





[illegible]









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Db 1093 GACACCTCTGGGGACCTGGTGAATCTCGCTACAGCTGACTTCCGAGCGACGAGCCT 1152
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Db 1153 TTGAATGGCGCAGTGAATGAGGCTCTCTCCCTGCTGAGTGACAGCAGTCTCGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaValPhe 420
Db 1213 GCTGAGCCAGTCCAGCTGAATCTCGCTGGCTGCTGGTGAATCTAGCCCTGGTTTTT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCTCTCTTTTGTGTCACAGCGTGGTCTCTCTGTCAGATGAGAGGCGACAGACA 1332
QY 441 ArgGlyThrIysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGTAGCGAGACTGGAGCC 1389

RESULT 7
LOCUS AR143487 1522 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6204370.
ACCESSION AR143487
VERSION AR143487.1 GI:15104773
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN gene and protein
JOURNAL Patent: US 6204370-A 1 20-MAR-2001;
FEATURES
Location/Qualifiers
1..1522
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 6 2e-103 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

US-09-967-237B-2 (1-459) x AR143487 (1-1522)
QY 1 MetAlaProLeuCysProSerProTyrLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGCCCTGTCTCAGGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACTGTGCAACTGTGCTGTCACTGCTCTCTGATGCTCTCCATCCCGAGAGTTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspProLeu 60
Db 133 CCCCCGATGAGGAGGATCCCCCTGGGAGGAGGCTCTTCTGGGGAAGATGATGCCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluAspProProGlyGlu 80
Db 193 GGCAGAGAGATCTGCCAGTGAAGAGGATTCACCCAGAGAGAGGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluAspLeuProGluValIysPro 100
Db 253 GAGATCTACTCTGAGAGGAGGATCTACCTGGAGAGGAGGATCTACTGAAGTTAGCCT 312
QY 101 LysSerGluGluGlySerLeuLeuLeuGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAAGAGGGCTCCCTGAAGTTAGAGATCTACTACTGTGTGAGGCTCTCTGGA 372
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QY 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspGlnSerHis 140
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QY 141 TrpArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCGCTATGAGGCGACCCCGCTGGCGCCCGGTGTCCCGACCTGCGCGCGCGCTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCCCGGTGGATATCCGCCCGCCAGCTCGCGCCCTTCTGCCGCCCTTGGCCCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200
Db 553 GAACCTCTGGCTTCCAGCTCCCGCGCTCCAGAACTGCGGCTCGCAACAATGSCCAG 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 613 AGTGTGCAACTGACCTGCTCTGGGTAGAGATGGCTCTGGGTCCCGCGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTyrGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 673 CGGGCTCTCGACCTGCATCTGCACCTGGGGGCTGCGAGTCTGTCGGGCTCGGAGCAC 732
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAGGCGACCGTTTCTCTGCGGAGATCCAGCTGTTCACTCAGCAGCCGCTTTGCC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACGAGCGCTTGGGGCGCCCGGAGGCGCTGCGCGTGTGTCGCGCTTTCTGGAG 852
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluIleAla 300
Db 853 GAGGGCCCCGGAAGAAACAGTGCCTATGAGCAGTTCTGTCTGCTTGGAAAGAAATCGCT 912
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGACTCAGGTCCCGAGCTGGACATATCTGCATCTCTCGCCCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTCAGCGCGTACTTCCATATGAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGGTG 1032
QY 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
Db 1033 ATCTGGACTGTGTATTAAACAGACAGTGTGTGAGTGCTAAGCAGCTCCACACCCCTCT 1092
QY 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTCTGGGACCTGTGACTCTCGGCTACAGCTGACTTCCGAGCGACGAGCCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGCGCAGTGAATGAGGCTCTCTCCCTGCTGAGTGACAGCAGTCTCGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaValPhe 420
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QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCTCTCTTTTGTGTCACAGCGTGGTCTCTCTGTCAGATGAGAGGCGACAGACA 1332
QY 441 ArgGlyThrIysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGTAGCGAGACTGGAGCC 1389

RESULT 8
LOCUS AR171392 1522 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6297041.
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ACCESSION  AR171392
VERSION     AR171392.1  GI:17910342
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 1522)
AUTHORS     Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE       MN gene and protein
JOURNAL     Patent: US 6297051-A 1 02-OCT-2001;
FEATURES    Location/Qualifiers
             1..1522
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Alignment Scores:
Pred. No.:      6.2e-103      Length:      1522
Score:          2424.00      Matches:    459
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:    100.0%      Indels:    0
DB:             6           Gaps:      0

US-09-967-237B-2 (1-459) x AR171392 (1-1522)

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DB 13 ATGGCTCCCTGTGCGCCAGCCCTGGCTCCTCTGTGATCCCGGCCCTGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 73 CTCACTGTGCAATGCTGCTGTCTACATGCTGCTTCTGATGCTCTCATCCCGAGAGGTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerProGlyGluAspProLeu 60
DB 133 CCCCAGATGACAGAGGATTCCTCCCTTGGAGAGGCTCTCTCTGGAGAGATGATGCCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
DB 193 GCGCAGAGGAGTCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
DB 253 GAGGATCTACTCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACTGAAGTTAAGCCT 312
QY 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
DB 313 AATACAGAGAGAGGCTCCCTGAGTTAGAGGATCTACTACTGTGAGGCTCCTGGA 372
QY 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
DB 373 GATCCTCAGAACCCAGAGATAATGCCACAGGACAAAGAGGGGATGACACAGAGTCAT 432
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DB 433 TGGCGCTATAGAGCGACCTCCCTGCCCCGGGTGTCCACAGCTGCGGGCGCGCTTC 492
QY 161 GlnSerProValAspLysArgProGlnLeuAlaPheCysProAlaLeuArgProLeu 180
DB 493 CAGTCCCGGTGATATCCCGCCCCCAGCTGCGCGCTTCTGCGCGGCTGCGCCCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAnglyHis 200
DB 553 GAACTCTCGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGGCTGCGGCAACATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
DB 613 AGTGTGCAACTGACCTTCCCTCTGGGCTAGAGATGCTCTGGGTCCTCGGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240
DB 673 CGGGCTCTGCAGCTGCATCTGCATCTGGGGGGCTGCAGGTCTCGGGCTCGGAGCACT 732

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QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu 280
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281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluLysAla 300
853 GAGGGCCCGAAGAAAACAGTGCTTATGAGCAGTTGCTGTCTCGCTTGAAGAAATCGCT 912
301 GluGluGlySerGluThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
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321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340
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381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
1153 TTGAATGGCGGAGTGTGATGAGGCTCTCTTCCCTGTGGAGTGGACAGCAGTCTCTCGGGCT 1212
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1273 GGCCTCTCTTTTGTGTCCACAGCGTCGCTTCTTGTGCAGATGAGAAGGCGACAGAGA 1332
441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
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RESULT 9
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DEFINITION Sequence 1 from patent US 6297051.
ACCESSION AR171563
VERSION AR171563.1 GI:17910513
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 1522)
TITLE Zavada,J., Pastorekova,S. and Pastorek,J.
JOURNAL MN gene and protein
FEATURES Patent: US 6297051-A 1 02-OCT-2001;
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ORIGIN
Alignment Scores:
Pred. No.:      6.2e-103      Length:      1522
Score:          2424.00      Matches:    459
Percent Similarity: 100.0%    Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match:    100.0%      Indels:    0
DB:             6           Gaps:      0

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US-09-967-237B-2 (1-459) x AR171563 (1-1522)

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Db 73 CTACCTGTGCACTGTCTGTCTACTGCTGCTTCTGATGCTCTCATCCCAAGAGTTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerGlyGlyAspAspProLeu 60
Db 133 CCCCAGATGCAGGAGATCCCTTGGGAGGAGCTCTTCTGGGAAGATGACCCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 193 GCGAGAGGAGATTCGCCATGAGAGGATTCACCCAGAGAGGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValHisPro 100
Db 253 GAGGATCTACCTGAGAGGAGATCTACCTGGAGAGGAGATCTACTGAGTTAGCCT 312
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QY 241 ValGluGlyHisArgPheProAlaGluIleHisValHisValHisSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGCTTCCCTGCGAGATCCAGTGTGTTCCCTCAGCACCGCTTTGGC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACAGGCGCTTGGGGCGCCCGGAGGCTGCGCGTGTGGCGCTTCTGGAG 852
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QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrProProCysAlaGlnGlyVal 340
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Db 1033 ATCTGGACTGTGTTTAACCAAGACAGTGTGCTGAGTGTCTAAGCAGTCTCCACACCTCTCT 1092
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QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAenPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGACCTGTGACTCTCGCTACAGTGTACTTCGAGGACGCGAGCT 1152
QY 381 LeuAenGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGCGAGTGATTGAGGCTCTCTTCCCTGCTGGAGTGACAGCAGCTCTCGGCT 1212
QY 401 AlaGluProValGlnLeuAenSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCCAGTCCAGTGAATTCCTGCTGGCTGGCTGTGGTGTGACATCTAGCCCTGGTTTT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTCTTTGCTGTACAGCGTCTGGCTGTCTTGTGACAGTGTGAGAGGACGACAGA 1332
QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGGAACCAAGGGGTGTGAGTACCGCCAGCAGAGGTAGCCGAGACTGGAGCC 1389

RESULT 10
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VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
OS Homo sapiens (human)
PN JP 2002528085-A/1
PD 03-SEP-2002
PF 22-OCT-1999 JP 2000578465
PR 23-OCT-1998 US 09/177776,23-OCT-1998 US 09/178115 PI
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C12N15/09, A61K38/00, A61K39/395, A61K39/395, A61K48/00, A61P35/00, PC
C07K14/47,
PC C12Q1/02, G01N33/566// (C12Q1/02, C12R1:91), C12N15/00, A61K37/02
CC MN gene and protein
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ORIGIN

Alignment Scores:
Pred. No.: 6,2e-103 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

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QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerGlyGlyAspAspProLeu 60
Db 133 CCCCAGATGCAGGAGATCCCTTGGGAGGAGCTCTTCTGGGAAGATGACCCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 193 GCGAGAGGAGATTCGCCATGAGAGGATTCACCCAGAGAGGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValHisPro 100
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QY 101 LysSerGluGluGlySerLeuLeuLeuGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAGAGAGGCTCCCTGAAGTTAGAGGATCTACTACTGTTAGGCTCTCTGGA 372
QY 121 AspProGlnGluProGlnAenAenAlaHisArgAspIysGluGlyAspAspGlnSerHis 140
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QY  
281 GluGlyProGluGluAenSerAlaTyrGluGlnLeuLeuSerArgLeuGluLysAla 300  
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853 GAGGGCCCGGAAGAAACAGTGCCTATAGCAGTTGCTGCTCGCTTGGAAAGAAATCGCT 912  
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Db  
913 GAGGAAGGCTCAGAGATCAGGTCCAGGATCCGACATATCTGCATCTCTGCGCTCTGAC 972  
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321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340  
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341 IleTrpThrValPheAenGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
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QY  
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Db  
1093 GACACCCCTGTGGGACCTGTGTGACTCTCGGCTACAGCTGAACCTTCGAGCGACGAGCCT 1152  
QY  
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QY 401 AlaGluProValGlnLeuAenSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
Db 1213 GCTGAGCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCTAGCCCTGGTTTTT 1272  
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440  
Db 1273 GGCCTCTTTTGTGTGTACACGCGTCCGCTTCTGTGAGATGAGAAGGCGACACAGA 1332  
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ACCESSION AR569592  
VERSION AR569592.1 GI:56570221  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 (bases 1 to 1522)  
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.  
TITLE MN gene and protein  
JOURNAL Patent: US 6770438-A 1 03-AUG-2004;  
Institute of Virology, Slovak Academy of Sciences; Bratislava;  
CXZ;  
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Db 73 CTCACGTGTCAACTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132  
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspProLeu 60  
Db 133 CCCCCGATGCAGAGGATTCCTCTGGGAGGAGGCTCTTCTGGGAAAGATGATCCCACTG 192  
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80  
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QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGlyGluAspLeuProGluValLysPro 100  
Db 253 GAGGATCTACTCTGGAGAGGAGGATCTACTCTGGAGAGGAGATCTACTCTGAAAGTTAAGCCT 312  
QY 101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120  
Db 313 AAATCAGAGAGAGGAGGCTCCCTGAAAGTTAGAGGATCTACTCTGAGGCTCTCTGGA 372  
QY 121 AspProGlnGluProGlnAenAenAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
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Db	733	GTGGAGGCCACCGTTTCCCTCCGAGATCCAGTGGTTCACCTCAGACCGCTTTGGC	792
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Db	793	AGAGTTGACGAGCGCTTGGGCGCCGGGAGGCTTGGCGTGTGGCCGCTTTCTGGAG	852
Qy	281	GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluLufLeAla	300
Db	853	GAGGGCCCGAAGAAACAGTGCTATGACAGTTCGTCTCGCTTGGAAAGAAATCGCT	912
Qy	301	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp	320
Db	913	GAGGAAGGCTCAGAGACTCAGTCCAGGACTGGACATATCTGCATCTCTGCCCTTGAC	972
Qy	321	PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal	340
Db	973	TTCCAGCGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGC	1032
Qy	341	IleTyrThrValPheAsnGlnThrValMetLeuSerAlaIysGlnLeuHisThrLeuSer	360
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Qy	361	AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro	380
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Qy	381	LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla	400
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Qy	401	AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe	420
Db	1213	GCTGAGCCAGTCCAGCTGAATCTCGCTGGCTGCTGGTGACATCTAGCCCTGGTTTTT	1272
Qy	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440
Db	1273	GGCTCTCTTTTCTGCTACACCGTCGCTTCTTGTGCAGATGAGAGGCGACAGAGA	1332
Qy	441	ArgGlyThrIysGlyGlyValserTyrArgProAlaGluValAlaGluThrGlyAla	459
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CQ834035			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
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ORGANISM			
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AUTHORS			
TITLE			
JOURNAL			
FEATURES			
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Alignment Scores:			
Pred. No.:			

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Db	103	CTACCTGTGCAACTGCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	162
Qy	41	ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu	60
Db	163	CCCCGGATGCAGAGGATTTCCCTTGGGAGGAGGCTCTTCTGGGGAAGATGACCCACTG	222
Qy	61	GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu	80
Db	223	GGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGATCCACCCGAGAG	282
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Qy	101	LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly	120
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Qy	121	AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis	140
Db	403	GATCTCTAAGAACCCAGAAATTAATGCCACAGGAGCAAAAGAGGGGATGACACAGATCAT	462
Qy	141	TyrArgTyrGlyGlyAspProTyrProArgValSerProAlaCysAlaGlyArgPhe	160
Db	463	TGGCGCTATGAGAGGCGACCCCGCTTGGCCCGGGTGTCCCGAGCTTGGCGGGCGCTTC	522
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Db	583	GAACTCTCGGGCTTCCAGCTCCCGCGCTCCAGAGACTCGCGCTCGCGCAACAAATGGCCAC	642
Qy	201	SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr	220
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Qy	221	ArgAlaLeuGlnLeuHisLeuHisTyrGlyAlaAlaGlyArgProGlySerGluHisThr	240
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Qy	241	ValGluGlyHisArgPheProAlaGluLleHisValValHisLeuSerThrAlaPheAla	260
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Qy	261	ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu	280
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Qy	281	GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluLufLeAla	300
Db	883	GAGGGCCCGAAGAAACAGTGCCTATGACAGTTCGTCTGCTGCTTGGAAAGAAATCGCT	942
Qy	301	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp	320
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DEFINITION Sequence 516 from Patent WO0194629.
ACCESSION AX330007
VERSION AX330007.1 GI:18102985
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Hominidae; Homo.
REFERENCE
1. Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horrihan, S., Soppet, D. R. and Weaver, Z.
Cancer gene determination and therapeutic screening using signature
gene sets
Avalon Pharmaceuticals (US)
Patent: WO 0194629-A 516 13-DEC-2001;
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283 GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCT 342
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141 TprArgTyrGlyGlyAspProTprProArgValSerProAlaCysAlaGlyArgPhe 160
463 TGGCGCTATGGAGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTGGCGGCGGCTTC 522
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523 CAGTCCCGGTGATATCCGCCCCAGCTGCGCGCTTCTGCCCGGCGCTTGGCGCCCTG 582
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201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
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221 ArgAlaLeuGlnLeuHisLeuHisTprGlyAlaAlaGlyArgProGlySerGluHisThr 240
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241 ValGluGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260
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1003 TTCAGCGCTACTTCCAATATGAGGGTCTCTGACTACACCGCTGTGCCAGGGGTGTC 1062
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361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAenPheArgAlaThrGlnPro 380
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381 LeuAenGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
1183 TTGATGGGCGAGTGTAGTGTAGGCTCTTCCCTGCTGAGTGTAGTGTAGTGTAGTGT 1242
401 AlaGluProValGlnLeuAenSerCysLeuAlaGlyAspIleLeuAlaLeuValPhe 420
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ACCESSION	AX332607		
VERSION	AX332607.1	GI:18123241	
KEYWORDS			
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		Hominidae; Homo.	
REFERENCE	1		
AUTHORS		Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,	
		Horgan, S., Soppet, D.R. and Weaver, Z.	
TITLE		Cancer gene determination and therapeutic screening using signature	
		gene sets	
JOURNAL		Patent: WO 0194629-A 3116 13-DEC-2001;	
		Avalon Pharmaceuticals (US)	
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DB:	6	Gaps:	0
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Db	103	CTCACTGTGCAACTGCTGTCTACTCTCTTGTATGCTGTCCATCCCCAGAGGTG	162
Qy	41	ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu	60
Db	163	CCCCGATGAGGAGGATTTCCCTCTGGAGGAGGCTCTTCTGGGAAGATGACCACTG	222
Qy	61	GlyGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu	80
Db	223	GGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGATCCACCGGAG	282
Qy	81	GluAspLeuProGlyGluGluAspLeuProGlyGlyGluAspLeuProGluValIysPro	100
Db	283	GAGGATCTACTGTGAGAGGAGGATCTACCTGGAGAGGAGGATTTACCTGAAGTTAAGCCT	342
Qy	101	LysSerGluGluGluGlySerLeuLeuLeuLeuGluAspLeuProThrValGluAlaProGly	120
Db	343	AAATCAGAAGAGGGCTCCCTGAAGTAGAGGATCTACTACTGTGTGAGGCTCTTGA	402
Qy	121	AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis	140
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Job time : 7268 secs

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

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Title: US-09-967-237b-2

Perfect score: 2424

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: Geneseqn2003as.\*  
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12: Geneseqn2004as.\*  
13: Geneseqn2004bs.\*  
14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	2424	100.0	1519	7 ADW41952	Adw41952 cDNA elev

5	2424	100.0	1522	2 AAT09186	Aat09186 MuTu puta
6	2424	100.0	1522	3 AAA16540	Aaa16540 Human MN
7	2424	100.0	1522	3 AAS2459	Aas2459 Human MN
8	2424	100.0	1522	12 ADG31413	Adg31413 Human MN
9	2424	100.0	1522	12 ADK41803	Adk41803 Human MN
10	2424	100.0	1522	14 ADZ64594	Adz64594 Human MN
11	2424	100.0	1552	6 ABL64779	Ab164779 Lung canc
12	2424	100.0	1552	6 ABL62179	Ab162179 Colon ade
13	2424	100.0	1552	6 ABL65416	Ab165416 Lung canc
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15	2424	100.0	1552	8 ABX76385	Abx76385 Lung canc
16	2424	100.0	1552	8 ABX76124	Abx76124 Lung canc
17	2424	100.0	1552	10 ADG89343	Adg89343 Cancer de
18	2424	100.0	1552	10 ACC72730	Acc72730 Human can
19	2424	100.0	1552	10 ABZ77284	Abz77284 Nucleotid
20	2424	100.0	1552	11 ADN39704	Adn39704 Cancer/an
21	2424	100.0	1552	11 ADN38987	Adn38987 Cancer/an
22	2424	100.0	1552	12 ADG31472	Adg31472 Human Car
23	2424	100.0	1552	12 ADQ17643	Adq17643 Human sof
24	2424	100.0	1552	12 ADQ29645	Adq29645 Human col
25	2424	100.0	1552	13 ADR24713	Adr24713 Breast ca
26	2424	100.0	1552	14 ADY61778	Ady61778 Human gen
27	2424	100.0	1658	12 ADQ22315	Adq22315 Human sof
28	2420	99.8	1552	13 ADQ87399	Adq87399 Human tum
29	2419	99.8	1833	4 AAH26551	Aah26551 DNA encod
30	2416	99.7	1572	14 AEA00062	Aea00062 Human TAT
31	2416	99.7	1572	14 AEA00582	Aea00582 Human TAT
32	2036	84.0	1397	2 AAQ48456	Aaq48456 MN CDNA c
33	1844.5	76.1	1089	12 ADL70159	Adl70159 Human car
34	1600	66.0	978	12 ADL70161	Adl70161 Glu-tagge
35	1596	65.8	1965	12 ADG31474	Adg31474 Murine ca
36	1576	65.0	978	12 ADL70163	Adl70163 Glu-tagge
37	1176.5	48.5	10897	2 AAT09187	Aat09187 MuTu puta
38	1176.5	48.5	10898	3 AAA16543	Aaa16543 Human MN
39	1176.5	48.5	10898	3 AAS2462	Aas2462 Human MN
40	1176.5	48.5	10898	12 ADG31415	Adg31415 Human MN
41	1176.5	48.5	10898	12 ADK41805	Adk41805 Human MN
42	1176.5	48.5	10898	12 ADP54001	Adp54001 Human car
43	1173.5	48.4	10898	14 ADZ64596	Adz64596 Human MN
44	1159	47.8	660	14 ACL57169	ACL57169 Human col
45	988	40.8	586	12 ADG31473	Adg31473 Human MN

#### ALIGNMENTS

RESULT 1  
ADL70155  
ID ADL70155 standard; cDNA; 1380 BP.  
XX  
AC ADL70155;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human carbonic anhydrase isozyme CA IX coding sequence.  
XX  
KW Human; carbonic anhydrase; tumour; antigen; cytosstatic; gene; aa.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1380  
FT /tag= b  
FT /product= "Carbonic anhydrase CA IX"  
FT sig\_peptide 1..110  
FT /tag= a  
FT mat\_peptide 111..1377  
FT /tag= c  
XX  
PN WO2004017923-A2.  
XX  
PD 04-MAR-2004.  
XX  
PF 25-AUG-2003; 2003WO-US026612.

```

XX
PR 23-AUG-2002; 2002US-0405577P.
PR 22-AUG-2003; 2003US-00646934.
XX
XX (CHIR ) CHIRON CORP.
XX
XX Wong J, Winter J, Lalehzadeh G, Warne R;
XX
XX WPI; 2004-226730/21.
XX P-PSDB; ADL70156.
XX
XX Identifying an agent capable of inhibiting carbonic anhydrase (CA)
XX activity of CA IX polypeptide for treating cancers, comprises combining a
XX test agent with a cell expressing CA IX and assessing CA inhibitory
XX activity of the test agent.
XX
XX Example 6; SEQ ID NO 1; 82pp; English.
XX
XX The present sequence is the coding sequence for human carbonic anhydrase
XX isozyme IX (CA IX), an N-glycosylated membrane-associated glycoprotein
XX also known as the MN or G250 tumour-associated antigen. The invention
XX relates to compositions and methods useful in inhibiting CA IX+
XX preneoplastic or neoplastic cells. The inhibitors are especially
XX antagonistic anti-CA IX antibodies and other inhibitory agents that
XX target the carbonic anhydrase activity of CA IX on these cells. The
XX antibodies, or their antigen-binding fragments, are specifically reactive
XX with an inhibitory epitope of CA IX. Screening assays for identifying
XX such inhibitory agents are provided. The antibodies, their antigen-
XX binding fragments, and other inhibitory agents are useful in the
XX treatment of cancers characterized by the expression of CA IX, such as:
XX head and neck cancers; gynaecological cancers including ovarian,
XX cervical, vaginal, endometrial and vulval cancers as well as
XX gynaecological precancerous conditions such as metaplastic cervical
XX tissues and condylomas; gastrointestinal cancers such as stomach, colon
XX and oesophageal cancers; urinary tract cancer such as bladder and kidney
XX cancers; skin cancer; liver cancer; prostate cancer; lung cancer; and
XX breast cancer.
XX
XX
SQ Sequence 1380 BP; 257 A; 428 C; 420 G; 275 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1,67e-130 Length: 1380
Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 12 Gaps: 0

US-09-967-237B-2 (1-459) x ADL70155 (1-1380)
QY 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeulleProAlaProGly 20
Dy 1 ATGGCTCCCTGTGCGCCAGCCCTGGCTCCCTCTGTGATGATCGCGCCCTGTCTCCAGGC 60
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Dy 61 CTCACTGTGCAACTGTCTGTCTCACTGCTCTTCTGATGCTCTGTCAATCCCGAGAGGTTG 120
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Dy 121 CCCCGGNTGAGAGAGNTTCCCTTGGGAGGAGGCTCTTCTGGGAGAGATGATCCCACTG 180
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
Dy 181 GCGCAGAGGAGGATGCGCCAGTGAAGAGGATTCACCCAGAGAGGAGGATCCACCCGAGAG 240
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGlyGluAspLeuProGluValLysPro 100
Dy 241 GAGGATCTACTCGAGAGGAGGATCTACCTGGAGAGGAGGATCTACTGAAGTTAAGCCT 300
QY 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Dy 301 AAATCAGAGAGAGGAGGCTCCCTGAGTTAGAGGATCTACTACTGTTTGGGGCTCTCTGGA 360

```

RESULT 2  
ADP54000  
ID ADP54000 standard; DNA; 1392 BP.  
XX

QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspGlyGlyGlyAspAspGlnSerHis 140  
Dy 361 GATCTCTCAAGAAACCCAGAAATAATGCCACAGGGGCAAAAGAGGGGATGACACAGTCTAT 420  
QY 141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160  
Dy 421 TGGCGCTATGGAGGGGACCCCGCTTGGCCCGGGGTGTCCCGAGCCTTGGCGGGCCGCTTC 480  
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180  
Dy 481 CAGTCCCGGTGGATATCCGCCAGCTCGCGCCTTCTGCGCGGCCCTTGCGGCCCTTG 540  
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200  
Dy 541 GAACTCTTGGGCTTCCAGCTCCCGCGCTCCAGAACTCGCGCTGCGCAACAATGGCCAC 600  
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220  
Dy 601 AGTGTCAACTGACCTGGCTCTCTGGGCTAGAGATGGCTCTGGGTCCCGGGCGGGAGTAC 660  
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240  
Dy 661 CGGGCTCTGCAGCTGCATCTGCACCTGGGGGGCTGCAGGTCTGTCGGGCTCGGAGCACACT 720  
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260  
Dy 721 GTGGAGGCGCCCGCTTTCCTCCGAGATCCAGTGGTTCACCTCAGCACCGCCTTTGCC 780  
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280  
Dy 781 AGATTGACAGGCTTGGGGGCGCCCGGAGGCTGGCCGTGTGGCCGCTTTCGGAG 840  
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuLeuSerArgLeuGluIleAla 300  
Dy 841 GAGGGCCCGAGAGAAACAGTGCCTATGACAGTTCGTCTGCTGCTTGAAGAAATCGCT 900  
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320  
Dy 901 GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCATCTCGCCCTCTGAC 960  
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340  
Dy 961 TTCAGCCGCTACTTCCCAATATGAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGGTGC 1020  
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
Dy 1021 ATCTGGACTGTGTGTTAAACAGACAGTGTGCTGAGTGTCTAAGCAGCTCCACACCTCTCT 1080  
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380  
Dy 1081 GACACCTGTGGGACCTCTGGTGACTCTCGGCTACAGCTGAACATTCGAGGAGCGAGCCT 1140  
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
Dy 1141 TTGAATGGGCGAGTGATTGAGGCTCTCTTCCCTGCTGGAGTGGACAGCAGCTCTCGGGCT 1200  
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
Dy 1201 GCTGAGCCAGTCCAGCTGAATCTCTCGCTGGGTGCTGCTGACATCTAGCCCTGGTTTTT 1260  
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgGlnHisArg 440  
Dy 1261 GGCTCTCTTTTGTCTGTACAGCGTCCGGTCTCTTGTGCGATGAGAGGCGAGCAGAGA 1320  
QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459  
Dy 1321 AGGGGACCAAGGGGGTGTGAGTACCGCCAGCAGAGAGTAGCCGAGACTGGAGCC 1377







Db 610 AGTGTGCAACTGACCTTCTCTGGCTAGAGATGGCTCTGGTCCCGGGGAGTAC 669  
Qy 221 ArgAlaLeuGlnLeuHisLeuHisThrProGlyAlaAlaGlyArgProGlySerGluHisThr 240  
Db 670 CGGGCTCTGCGAGTGCATCTGCACATCGGGGGCTGCAGGTCTGCGGGCTCGGAGCACAT 729  
Qy 241 ValGluGlyHisArgPheProAlaGluLeuHisValValHisLeuSerThrAlaPheAla 260  
Db 730 GTGGAAGGCCACCGTTTCCCTGCGAGATCCAGTGGTTCACCTCAGCACCGCTTTGGCC 789  
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu 280  
Db 790 AGAGTTGACGAGGCCCTTGGGGCCCGGGAGGCTGCGCGTGTGGCCGCTTTCTGGAG 849  
Qy 281 GluGlyProGluLeuAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluLeuAla 300  
Db 850 GAGGGCCCGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTGAAGAATAATCGCT 909  
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspLeuSerAlaLeuLeuProSerAsp 320  
Db 910 GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGCACATATCTGCATCTCTGCCCTCTGAC 969  
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340  
Db 970 TTCAGCGCTACTTCCAAATAGAGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGT 1029  
Qy 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
Db 1030 ATCTGGACTGTGTTAAACACAGACAGTGTGCTGAGTGAAGCAGCTCCACACCTCTCT 1089  
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380  
Db 1090 GACACCTGTGGGACCTGTGACTCTCGCTACAGCTGAACATTCGAGGAGCGACGCT 1149  
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400  
Db 1150 TTGAATGGGCGAGTGATGAGGCTCTTCCCTGCTGGAGTGACAGCAGTCTCGGGCT 1209  
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
Db 1210 GCTGAGCCAGTCCAGCTGAATCTCGCTGGCTGCTGCTGACATCTAGCCCTGGTGT 1269  
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440  
Db 1270 GGCTCTCTTTTGTGTGCACAGCGTCCGCTTCTTGTGCAGATGAGAGGCGACAG 1329  
Qy 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyVal 459  
Db 1330 AGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGTAGCCGAGACTGGAGCC 1386  
RESULT 4  
ID ADW41952 standard; cDNA; 1519 BP.  
XX AC ADW41952;  
XX AC  
XX DT 24-MAR-2005 (first entry)  
XX DE cDNA elevated in kidney tumor cells SEQ ID NO 1695.  
XX KW gene therapy; diagnosis; pharmaceutical; cancer; cytostatic;  
XX KW genitourinary disease; neoplasm; renal tumor; gene; ss.  
XX OS Unidentified.  
XX PN W0200274237-A2.  
XX PD 26-SEP-2002.  
XX PF 19-MAR-2002; 2002WO-US010055.  
XX PR 19-MAR-2001; 2001US-0277245P.

PR 21-DEC-2001; 2001US-0343340P.  
XX (CORI-) CORIXA CORP.  
XX PA Algate PA, Mannion J, Gaiger A, Gordon B, Harlocker SL;  
XX WPI; 2002-759855/82.  
XX New isolated polynucleotides and polypeptides, useful for detecting the  
PT presence of, and treating cancer, particularly kidney cancer by  
PT stimulating T-cells specific for a tumor protein, and stimulating immune  
PT response in a patient.  
XX Claim 13; SEQ ID NO 1695; 252bp; English.  
XX The invention describes a new isolated polynucleotide (I) comprising: any  
CC one of the 185 sequences identified in the specification; complements or  
CC degenerate variants of (a); sequences consisting of at least 20  
CC contiguous residues of (a); sequences that hybridize to (a) under highly  
CC stringent conditions; or sequences having at least 75 or 90% sequence  
CC identity to (a). Also described are: detecting (M1) or determining the  
CC presence of cancer in a patient; stimulating (M2) an immune response in a  
CC patient; treating (M3) kidney cancer in a patient; an isolated  
CC polypeptide (II) encoded by (I) and comprising, or having at least 70 or  
CC 90% sequence identity to, any one of the 8 sequences identified in the  
CC specification; an expression vector (III) comprising (I) operably linked  
CC to an expression control sequence; a host cell (IV) transformed or  
CC transfected with (III); an isolated antibody (V) or its antigen-binding  
CC fragment that specifically binds to (II); a fusion protein (VI)  
CC comprising at least one (II); an oligonucleotide (VII) that hybridizes to  
CC the nucleotide sequences cited above under highly stringent conditions;  
CC stimulating (M4) and/or expanding T-cells specific for a tumor protein;  
CC an isolated T-cell population (VIII) comprising the T-cells in (M4); a  
CC composition (IX) comprising a first component such as a carrier or  
CC immunostimulant and a second component comprising (I), the polypeptide  
CC encoded by (I), an antibody or its antigen-binding fragment that  
CC specifically binds to (II), (VI), or an antigen-presenting cell that  
CC expresses the polynucleotide; and a diagnostic kit (X) comprising at  
CC least one of the oligonucleotide, or at least one antibody and a  
CC detection reagent comprising a reporter group. The polynucleotides,  
CC polypeptides, antibodies and antigen-presenting cells are useful for  
CC detecting the presence of, and treating cancer, particularly kidney  
CC cancer by stimulating and/or expanding T-cells specific for a tumor  
CC protein, and stimulating immune response in a patient. This sequence  
CC represents a kidney tumour cDNA, expression of which is increased in  
CC kidney tumors.  
XX SQ Sequence 1519 BP; 296 A; 456 C; 453 G; 314 T; 0 U; 0 Other;  
Alignment Scores:  
Pred. No.: 1,84e-130 Length: 1519  
Score: 2424.00 Matches: 459  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0  
US-09-967-237B-2 (1-459) x ADW41952 (1-1519)  
Qy 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuLeuProAlaProGly 20  
Db 10 ATGGCTCCCTGTGCCCGCCAGCCCTGGCTCCCTCTGTGATCCCGCCCTGTCCAGGC 69  
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40  
Db 70 CTCACCTGTGCACCTGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 129  
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerGlyGlyGlyGlyGlyGlyGly 60  
Db 130 CCCCCGATGACGAGGATTTCCCTTGGGGGAGGCTCTTCTGGGGAAGATGATCCACTG 189  
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80

Db 190 GCGAGAGGAGATCTGCCAGTGAAGAGGATTCTCCAGAGAGGAGGATCCACCCGGAGAG 249  
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100  
Db 250 GAGGATCTACTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACTGAAGTTAGCCT 309  
Qy 101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120  
Db 310 AAATCAGACAGAGAGGCTCCCTCAAGTTAGAGGATCTACTACTGTTGAGGCTCTCGGA 369  
Qy 121 AspProGlnGluProGlnAenAenAlaHisArgAspLysGluGluAspAspGlnSerHis 140  
Db 370 GATCCTCAAGACCCCAAGATAATGCCACAGGACAAAGAGGAGGATGACCAAGTGCAT 429  
Qy 141 TrpArgTyrglyGlyAspProProTtpProArgValSerProAlaCysAlaGlyArgPhe 160  
Db 430 TGGCGCTATGAGGCGACCCGCCCTGGCCCCGGGTGTCCCCAGCCTCGCGGGCCGCTTC 489  
Qy 161 GlnSerProValAspLeuArgProGlnLeuAlaAAlaPheCysProAlaLeuArgProLeu 180  
Db 490 CAGTCCCGGTGGATATCCGCCCCAGCTCGCGCCCTTCTGCCCGGCGCTGCGCCCGCTG 549  
Qy 181 GluLeuLeuGlyPheGlnLeuProLeuProGluLeuArgLeuArgAenGlyHis 200  
Db 550 GAATCTCTGGGCTTCAGCTCCCGCGCTCCCAAGACTGGCGCTGCGCAACATGGCCAC 609  
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220  
Db 610 AGTGTGCAACTGACCTGCCCTCTGGGCTAGAGATGGCTCTGGGTCCCGGGGGAGTAC 669  
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAglArgProGlySerGluHisThr 240  
Db 670 CCGGCTCTGCAGCTGCATCTGCATCTGGGGGCTGCAGGTCTCGCGGCTCGGAGCACACT 729  
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260  
Db 730 GTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGTGGTTCACCTCAGCACCGCTTGTCC 789  
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280  
Db 790 AGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTTGGCGGTGTGGCGGCTTCTCGGAG 849  
Qy 281 GluGlyProGluGluAenSerAlaTyrGluGlnLeuLeuSerArgLeuGluIleAla 300  
Db 850 GAGGGCCCGGAAGAAACAGTGCCTATGACAGTTCGTCTGCTTGAAGAAATCGCT 909  
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspLysAlaLeuLeuProSerAsp 320  
Db 910 GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCATCTCGCCCTCTGAC 969  
Qy 321 PheSerArgTyrglyPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340  
Db 970 TTCAGCGGCTACTTCCAATATGAGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGT 1029  
Qy 341 IleTrpThrValPheAenGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
Db 1030 ATCTGAGCTGTGTTTAACACAGACAGTGTCTGAGTGTCTAAGCAGCTCCACACCTCTCT 1089  
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAenPheArgAlaThrGlnPro 380  
Db 1090 GACACCTGTGGGAGCTGTGGTACTCTGGCTACAGTGAATCTCGAGGCGAGCGGCT 1149  
Qy 381 LeuAenGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
Db 1150 TTCAATGGGGAGTGTGAGGCTCTCTTCCCTGCTGGAGTGCAGCAGCAGTCTCGGGCT 1209  
Qy 401 AlaGluProValGlnLeuAenSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
Db 1210 GCTGAGCCAGTCCAGCTGAATTCCTCGCTGGCTGCTGGTGCATCTCAGCCCTGGTTTTT 1269  
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440  
Db 1270 GGCCTCTTTTGTGTCCACGCGTCCGCTTCTTGTGCAGATGAGAGGCGAGCACAGA 1329

Qy 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459  
Db 1330 AGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACTGGAGCC 1386  
RESULT 5  
AAT09186  
ID AAT09186 standard; cdNA; 1522 BP.  
XX  
AC AAT09186;  
XX  
DT 25-MAR-2003 (revised)  
DT 19-AUG-1996 (first entry)  
XX  
DE MuTu putative oncogene MN cdNA.  
XX  
XX MuTu; endogenous; cellular component; MN; HeLa cell; diagnosis;  
XX lymphocytic choriomeningitis virus; LCMV; putative oncogene; treatment;  
XX neoplastic; pre-neoplastic; disease; anticense therapy; antibody;  
XX vaccine; vertebrate; immunisation; ss.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
PH 13..1392  
FT CDS /\*tag= a  
XX  
XX W09534650-A2.  
XX  
XX 21-DEC-1995.  
XX  
XX 15-JUN-1995; 95WO-US007628.  
XX  
XX 15-JUN-1994; 94US-00260190.  
PR 07-JUN-1995; 95US-00477504.  
PR 07-JUN-1995; 95US-00481658.  
PR 07-JUN-1995; 95US-00485049.  
PR 07-JUN-1995; 95US-00485862.  
PR 07-JUN-1995; 95US-00485863.  
PR 07-JUN-1995; 95US-00486756.  
PR 07-JUN-1995; 95US-00487077.  
XX  
XX (CIBA ) CIBA CORNING DIAGNOSTICS CORP.  
PA (VIRO-) INST VIROLOGY.  
XX  
PI Zavada J, Pastorekova S, Pastorek J;  
XX  
XX WPI; 1996-049679/05.  
DR P-PSDB; AAR88058.  
XX  
XX MN gene, protein and nucleic acid fragments - used as primers and probes  
PT in the detection of MN antigens and antibodies, and in the treatment of  
PT (pre)neoplastic disease.  
XX  
XX Claim 1; Fig 1; 102pp; English.  
XX  
XX The present sequence is the full length MuTu endogenous cellular  
CC component, MN, cdNA clone, which was isolated from lymphocytic  
CC choriomeningitis virus (LCMV) infected HeLa cells. Persistent LCMV, the  
CC exogenous MuTu transmissible agent (MX), infection increases the  
CC expression level of the MN gene. MN is a putative oncogene, and can  
CC therefore be used in the development of prods. for the diagnosis and  
CC treatment of neoplastic (NP), or pre-NP diseases. NP diseases can be  
CC treated using DNA antisense to MN transcribed mRNA, anti-MN protein  
CC antibodies can be used for the diagnosis NP or pre-NP diseases and a  
CC vaccine contg. immunogenic amounts of the MN protein can be used to  
CC immunise a vertebrate against a NP disease associated with MN antigen  
CC expression. (Updated on 25-MAR-2003 to correct PR field.)  
XX  
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;  
Alignment Scores: 1.85e-130 Length: 1522  
Pred. No.:



CC The present invention describes a method of screening for  
 CC preneoplastic/neoplastic disease. The method comprises: (1) determining  
 CC whether abnormal MN gene expression is present in a vertebrate; and (2)  
 CC if abnormal MN gene expression is determined to be present in the  
 CC vertebrate, determining that the vertebrate has a significant risk of  
 CC having preneoplastic/neoplastic disease. The MN gene is an oncogene and  
 CC encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN  
 CC protein is a tumour associated carbonic anhydrase isoenzyme. The method  
 CC is used for detecting a wide variety of preneoplastic/neoplastic diseases  
 CC in a vertebrate, preferably a human. The disease detected is mammary,  
 CC bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,  
 CC vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,  
 CC testicular, brain, head and neck, mesodermal, gallbladder, rectal,  
 CC duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric  
 CC mucosa, gallbladder epithelium, small intestinal mucosa, colorectal  
 CC mucosa, pancreatic duct epithelium or liver duct epithelium  
 CC preneoplastic/neoplastic disease. AAAL6540 to AAAL6617 and AAY53228 to  
 CC AAY53245 represent sequences used in the exemplification of the present  
 CC invention

XX  
 SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1-85e-130 Length: 1522  
 Score: 2424.00 Matches: 459  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 3 Gaps: 0

US-09-967-237B-2 (1-459) x AAAL6540 (1-1522)

QY 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuLeuLeuProLaProLaProGly 20  
 DB 13 ATGGCTCCCTGTGCCCGCCAGCCCTGGCTCCCTGTGATCCCGGCCCTGTCCAGGC 72  
 QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40  
 DB 73 CTACATGTGCACTGTGCTGTCTACATGTGCTGTCTGTGATCCCGAGGGTTG 132  
 QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspProLeu 60  
 DB 133 CCCCCGATGACAGAGGATTCCTCCCTGGGAGGAGGCTCTTCTGGGAGAGTACCCACTG 192  
 QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80  
 DB 193 GCGCAGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGATCCACCCGAGAG 252  
 QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluVallysPro 100  
 DB 253 GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCT 312  
 QY 101 LysSerGluGluGlySerLeuLeuLysLeuGluAspLeuProThrValGluAlaProGly 120  
 DB 313 AAATCAGAGAGAGAGGCTCCCTGAGTTAGAGGATCTACCTACTGTTGAGGCTCTCGA 372  
 QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
 DB 373 GATCTCTAAGAACCCAGAAATAATGCCACAGGACAAAGAGGGGATGACACAGAGTCAT 432  
 QY 141 TrpArgTyrGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160  
 DB 433 TGGCGCTATGGAGGCGACCCCTCGCCCCGGGTGTCCCGAGCTGCGCGGCGCGCTTC 492  
 QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180  
 DB 493 CAGTCCCGGTGGATATCCGCCGCCCTCGCGCTTCGCCCCGCCCTCTGCGCCCCCTG 552  
 QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200  
 DB 553 GAACTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGGCTGCGCAACAATGGCCAC 612  
 QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220

DB 613 AGTGTGCAACTGACCCCTGCTCTGCGCTAGAGATGGCTCTGCGTCCCCGGCGGAGTAC 672  
 QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240  
 DB 673 CGGGCTCTGCGAGTGCATCTGCACCTGGGGGGCTGCAGGTCGTCCGGGCTCGGAGCACACT 732  
 QY 241 ValGluGlyHisArgPheProAlaGluLleHisValValHisLeuSerThrAlaPheAla 260  
 DB 733 GTGGAGGCGCACCGTTCCTCCCGAGATCCACGTGGTTTCACCTCAGCACCGCTTTGGC 792  
 QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280  
 DB 793 AGATTGACAGGCTTTGGGGCGCCCGGAGAGGCTGGCGGTGTGGCCGCCCTTTCTGGAG 852  
 QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluLeuAla 300  
 DB 853 GAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTTGCTGTCTCGCTTGAAGAAATCGCT 912  
 QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320  
 DB 913 GAGGAAGGCTCAGAGACTCAGGTCCCGAGACTGGACATATCTGCATCTCTGCCCTCTGAC 972  
 QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340  
 DB 973 TTCAGCGGCTACTTCCATATGAGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGTCT 1032  
 QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
 DB 1033 ATCTGGACTGTGTTAAACCAGACAGTGTGCTGAGTGTCTAAGCAGCTCCACACCCCTCTCT 1092  
 QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380  
 DB 1093 GACACCTGTGGGACCTGTGCTGACTCTCGCTACAGCTGAACTTCGAGACGACGACCT 1152  
 QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
 DB 1153 TTGAATGGCGAGTGTATGAGGCTCTCTTCCTCTGCTGGAGTGGACAGCAGTCTCTGGGCT 1212  
 QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
 DB 1213 GCTGAGCCAGTCCAGCTGAATTCCTGCCCTGGCTGTGCTGGTGACATCTAGCCCTGGTTTT 1272  
 QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgGlnHisArg 440  
 DB 1273 GGCCTCTCTTTTGTCTGTCACAGCGTCGCGTTCTTGTGTCAGATGAGAGGCGACAG 1332  
 QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459  
 DB 1333 AGGGGNACCAAGGGGGTGTGAGCTACCGCCCGACAGAGGTAGCCGAGACTGGAGCC 1389

RESULT 7  
 AAA52459  
 ID AAA52459 standard; cDNA; 1522 BP.  
 XX  
 AC AAA52459;  
 XX  
 DT 25-SEP-2000 (first entry)  
 XX  
 DE Human MN cDNA.  
 XX  
 KW MN protein; tumour associated cell adhesion molecule; oncoprotein;  
 KW proteoglycan domain; PG domain; carbonic anhydrase; CA domain;  
 KW abnormal expression; neoplastic disease; cancer; gene therapy; ss.  
 OS Homo sapiens.  
 XX  
 PH Location/Qualifiers  
 FT 13..1392  
 FT /\*tag= a  
 FT /product= "Human MN protein"  
 XX  
 PN W020024913-A2.



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|||||
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QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCTCTCTTTTCTGCTGTCACAGCGTGGGTTCTTGTGCGAGATGAGAGGCGACACAGA 1332
QY 441 ArgGlyThrIysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGAAACCAAGGGGTGTGTAGTACCGCCAGCAGAGGTAGCCGAGAGTGGAGCC 1389

RESULT 8
ADG31413
ID ADG31413 standard; cDNA; 1522 BP.
XX AC ADG31413;
XX DT 26-FEB-2004 (first entry)
XX DE Human MN cDNA SeqID 1.
XX KW human; gene; ss; monoclonal antibody; MN/CA IX; MN; oncogene;
KW carbonic anhydrase 9; CA9; MN/CA9; carbonic anhydrase IX; CA IX; MN/G250;
KW neoplastic tumour; cytostatic; cancer; tumour therapy;
KW anti-tumour vaccine.
XX OS Homo sapiens.
XX PN WC2003100029-A2.
XX XX 04-DEC-2003.
XX 22-FEB-2003; 2003WO-US0005136.
XX 23-MAY-2002; 2002US-0383068P.
PR 05-DEC-2002; 2002US-0431499P.
XX (FARB ) BAYER CORP.
PA (VIRO-) INST VIROLOGY.
XX Pastorek J, Pastorekova S, Zatovicova M, Zavada J, Ortova Gut M;
XX WPI; 2004-0351136/03.
DR P-PSDB; ADG31414.
XX New monoclonal antibody generated from MN/CA IX-deficient mice, where the
PT antibody binds specifically to human tumor-associated cell adhesion
PT protein MN/CA IX or polypeptide, useful for diagnosing, prognosing or
PT treating cancer.
XX Disclosure; SEQ ID NO 1; 156pp; English.
XX This invention relates to a novel monoclonal antibody identified as the
CC MN/CA IX specific antibody prepared in knockout mice (CA IX deficient
CC mice). Specifically, this antibody is directed towards the MN gene, a
CC cellular oncogene known alternatively as carbonic anhydrase 9, CA9 or
CC MN/CA9, which encodes the MN protein that is also known as the MN/CA IX
CC isoenzyme, carbonic anhydrase IX, CA IX or the MN/G250 protein. The
CC present invention describes the generation of this monoclonal antibody,
CC and immunoreactive fragments thereof, which are directed against non-
CC immunodominant epitopes on the CA IX extracellular domain. As such, this
CC antibody can be useful diagnostically as a marker for preneoplastic/
CC neoplastic tumours, immunodetection methods and immunotargeting
CC approaches. Accordingly, compositions exhibit cytostatic activity and are
CC useful in the diagnosis, prognosis and treatment of various cancers
CC including breast, bladder or lung cancer, in tumour therapy and in anti-
CC tumour vaccination. This polynucleotide sequence is the human MN cDNA of
CC the invention.
XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.85e-130 Length: 1522
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Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 12 Gaps: 0
US-09-967-237B-2 (1-459) x ADG31413 (1-1522)
QY 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTCTGTGATCCCGCCCTGTCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGTCAACTGCTGTCTGCTGCTTCTGATGCTGTCTCATCCCCAGAGGTTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspProLeu 60
Db 133 CCCCCGATCGAGGAGGATTTCCCTTGGAGGAGGCTCTTCTGGGGAAGATGACCCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 193 GCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValIysPro 100
Db 253 GAGGATCTACTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACTGAAGTTAAGCCT 312
QY 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAGAGAGGGGCTCCCTGAAGTTAGAGGATCTACTACTCTTGAGGCTCTCGA 372
QY 121 AspProGlnGluProGlnAenAenAlaHisArgAspLysGlyGlyAspAspGlnSerHis 140
Db 373 GATCTCTCAAGAACCCCCAGAAATAATGCCACAGGACAAAGAGAGGATGACACAGTCA 432
QY 141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCGCTATGGAGGGCGACCCCGCTTGGCCCGGGTGTCCCGAGCTTGGCGGGCGCGCTT 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCCGGTGGATATCCGCCCCAGCTCGCGCGCTTCTGCCCGGCCCTTGGCCCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAenAnglyHis 200
Db 553 GAACTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCGCTGCGCAACAATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 613 AGTGTGCAACTGACCTGCTCTGGGCTTAGAGATGGCTTGGGTCCCAGGCGGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 673 CGGGCTCTCGAGCTGATCTGCACTGGGGGGCTGCAAGTCTGTCGGGCTCGAGACACT 732
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAGGGCCACCGTTTCCCTGCGGAGATCCACGTGGTTCACCTCAGCACCGCGCTTTGCC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACAGAGGCTTTGGGGGCCCGGGAGGCGCTGGCCGTGTTCGCCCTTCTGGAG 852
QY 281 GluGlyProGluGluAenSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
Db 853 GAGGGGCCCGAGAGAAAACAGTGCCTATGACAGTTCGTCTGCTTGGAGAGAAATCGCT 912
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGACTCAGGTCCCGAGACTGGACATATCTGCACTCTCGCCCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGlySerLeuThrThrProProCysAlaGlnGlyVal 340
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Db 973 TTTCAGCGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGTGCCCAGAGGTGTC 1032  
Qy 341 lletftrpThValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
Db 1033 APTCGACTGTGTTTAAACACAGACAGTGATGCTGAGTGTCTTAACAGCTCCACACCTCTCT 1092  
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380  
Db 1093 GACACCTGTGGGACCTGTGTACTCTCGCTACAGCTGAACTTCGAGCGACGAGCT 1152  
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
Db 1153 TTGAATGGCGAGTGATTGAGGCTCTCTCCCTGCTGGAGTGACAGCAGTCTCTGGGCT 1212  
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
Db 1213 GCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGTGCTGTGAGATCTAGCCCTGTGTTT 1272  
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440  
Db 1273 GGCCCTCTTTTGTGTACACGCGTCCGCTTCTTGTGCAGATGAGAAAGGCAGACAGA 1332  
Qy 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459  
Db 1333 AGGGGACCCAAAGAGGGTGTGAGTACCCTCCAGCAGAGTAGCCGAGACTGGAGCC 1389

RESULT 9  
ADK41803

ID ADK41803 standard; DNA; 1522 BP.

XX ADK41803;

XX 06-MAY-2004 (first entry)

XX Human MN gene sequence SeqID1.

XX carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;  
KW human; vertebrate; cytostatic; vaccine; gene therapy;  
KW renal cell carcinoma; breast cancer; colorectal cancer; ds; gene.  
XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 13..1392

FT /\*tag= a

FT /product= "Human MN protein"

XX WO2004/005348-A1.

XX 15-JAN-2004.

XX 22-FEB-2003; 2003WO-US005137.

XX 23-MAY-2002; 2002US-0383068P.

XX 05-DEC-2002; 2002US-0431499P.

XX (FARB ) BAYER CORP.

XX (VIRO-) INST VIROLOGY.

XX Zavada J, Pastorekova S, Pastorek J, Zavadova Z;

XX WPI; 2004-083500/08.

XX P-PSDB; ADK41804.

XX New soluble form of the carbonic anhydrase IX (CA IX) protein for  
PT screening, diagnosing or prognosing diseases associated with abnormal  
PT expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or  
PT colorectal cancer.

XX Disclosure; SEQ ID NO 1; 159pp; English.

XX This invention relates to a novel soluble form of the carbonic anhydrase

CC IX (CA IX) (or MN) protein or CA IX polypeptide which is released from  
CC precancerous and/or cancerous cells of a vertebrate into a body fluid.  
CC The invention may be useful for the development of compounds with a  
CC cytostatic activity or a vaccine whilst the disclosed sequences may be  
CC used for gene therapy. The protein and method are useful for screening of  
CC diagnosing or prognosing diseases associated with abnormal expression of  
CC carbonic anhydrase IX protein, such as precancerous and cancerous  
CC diseases like renal cell carcinoma, breast cancer or colorectal cancer.  
CC The monoclonal antibody may also be used for treating or preventing  
CC precancerous and cancerous diseases. The present sequence is that of the  
CC gene which encodes the human MN protein of the invention.

XX Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,85e-130 Length: 1522  
Score: 2424.00 Matches: 459  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 12 Gaps: 0

US-09-967-237B-2 (1-459) x ADK41803 (1-1522)

Qy 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuLeuProAlaProAlaProGly 20  
Db 13 ATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTTGATCCCGGCCCTGCTCCAGGC 72  
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40  
Db 73 CTCACGTGTCAACTGCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132  
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu 60  
Db 133 CCCCAGATGTCAGAGGATTCCTCCCTTTGGAGAGAGGCTCTTCTGGGAAGATGACCCACTG 192  
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80  
Db 193 GCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGATCCACCCGAGAGAG 252  
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100  
Db 253 GAGGATCTACCTGGAGAGAGGATCTACCTGGAGAGAGGATCTACCTGAAGTTAAGCCT 312  
Qy 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120  
Db 313 AAAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTGAGGCTCTCTGA 372  
Qy 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
Db 373 GATCTCTAAGAACCCAGAGATATGCCCCACAGGACAAAGAGGGGATGACCCAGAGTCAT 432  
Qy 141 TrpArgTyrGlyGlyAspProTrpProArgValSerProAlaCysAlaGlyArgPhe 160  
Db 433 TGGCGCTATGGAGGCGACCCGCTGGCCCGCGGTGTCCCGAGCTGCGCGGCGCGCTTC 492  
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180  
Db 493 CAGTCCCCGGTGGATATCGCCCCCAGCTCGCCGCTCTTTCGCCGCCCTCGGCCCTCTG 552  
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlnHis 200  
Db 553 GAACTCTCTGGGCTTCCAGCTCCCGCGCTCCCGAGAACTGCGGCTGGCAACATGSCCAG 612  
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220  
Db 613 AGTGTGCAACTGACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 672  
Qy 221 ArgAlaLeuGlnLeuHisLeuHisThrGlyAlaAlaGlyArgProGlySerGluHisThr 240  
Db 673 CGGGCTCTGCAGCTGCATCTGCACCTGGGGGGCTGAGAGGTGCTCGGGGCTCGGAGCAACT 732  
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260



Db	733	GTGGAGGGCCACCGTTTCCCTGCCGAGATCCACGTGTTTACCTCAGCACCGCGCTTTGGC	792
QY	261	AtgValaspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu	280
Db	793	AGAGTTGACGAGGCCCTTGGGCGCCCGGAGGCGCTGGCCGTGTGGCCGCTTTCGGAG	852
QY	281	GluGlyProGluGluAenSerAlaTyTyGluGlnLeuLeuSerArgLeuGluGluLeAla	300
Db	853	GAGGGCCCGAAGAAACAGTCTATGAGCAGTTGCTGCTCGCTTGAAGAANAATCGCT	912
QY	301	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuProSerAsp	320
Db	913	GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGACATATCTGCATCTCGCCCTCTGAC	972
QY	321	PheSerArgTyTyPheGlnTyTyGluGlySerLeuThrProProCysAlaGlnGlyVal	340
Db	973	TTGAGCGGCTACTTCCATATAGAGGGGTCTCTGACTACACCGGCTGTGCCAGGGTGTC	1032
QY	341	IleTrpThrValPheAenGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer	360
Db	1033	ATCTGACTGTGTAAACACAGACAGTGATGCTGAGTGCTAAGCAGCTCCACACCCCTCTCT	1092
QY	361	AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro	380
Db	1093	GACACCCCTGTGGGACCTGTGACTCTCGGCTACAGCTGAACCTCCGAGCGCAGCCT	1152
QY	381	LeuAenGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla	400
Db	1153	TTGAATGGGCGAGTGATTTGAGGCTCTCTCCCTGCTGGAGTGACAGCTCTCGGGT	1212
QY	401	AlaGluProValGlnLeuAenSerCysLeuAlaAlaGlyAspIleLeuAlaValPhe	420
Db	1213	GCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGCTGGTGACATCTAGCCCTGGTTTT	1272
QY	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440
Db	1273	GGCCTCTTTTGTCTGTCACAGCGTCGCGTTCCTTTGTGAGATGAGAAGGCACACAGA	1332
QY	441	ArgGlyThrLysGlyGlyValSerTyTyArgProAlaGluValAlaGluThrGlyAla	459
Db	1333	AGGGGAACCAAGGGGTGTGAGCTACCGCCGACGAGAGTAGCCGAGCTGGAGCC	1389
RESULT 10			
ADZ64594			
ID	ADZ64594 standard; cDNA; 1522 BP.		
XX			
AC	ADZ64594;		
XX			
DT	14-JUL-2005 (first entry)		
XX			
DE	Human MN/CA IX cDNA.		
XX			
KW	Prognosis; oncogene; neoplasm; MN/CA IX; stomach tumor;		
KW	gallbladder disease; biliary cancer; biliary tumor; testis tumor;		
KW	ovary tumor; basal cell carcinoma; central nervous system tumor; gene;		
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OS	Homo sapiens.		
XX			
FH	Key Location/Qualifiers		
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FT	/*tag= a		
FT	mat_peptide 124..1389		
FT	/*tag= c		
FT	/product= "Mature MN/CA IX"		
XX			
PN	WO2005037083-A2.		
XX			
PD	28-APR-2005.		

XX	18-OCT-2004; 2004WO-US034573.		
PF			
XX	16-OCT-2003; 2003US-0511832P.		
PR			
XX	(FARB ) BAYER HEALTHCARE.		
PA	(VIRO-) INST VIROLOGY.		
PA			
XX	Ebert M, Rocken C, Pastorekova S, Zavada J, Pastorek J;		
PI			
XX	WPI: 2005-315588/32.		
DR	P-PSDB; ADZ64595.		
DR			
XX			
PT	Prognosticating preneoplastic/neoplastic diseases of the breast.		
PT	gallbladder, biliary ducts, testis or ovaries, by detecting MN/CA9 gene		
PT	expression products, useful in medical genetics, biochemical engineering		
PT	and immunochemistry.		
XX			
PS	Claim 1; SEQ ID NO 1; 83pp; English.		
PS			
XX	The invention relates to a method of prognosticating a		
CC	preneoplastic/neoplastic disease afflicting a subject vertebrate, where		
CC	the disease affects a tissue that normally expresses an MN/CA IX protein		
CC	but loses or has significantly reduced MN/CA IX expression upon		
CC	carcinogenesis, comprising detecting an MN/CA9 gene expression product in		
CC	a sample having preneoplastic/neoplastic tissue taken from the		
CC	vertebrate, quantitating the level of the MN/CA9 gene expression product in		
CC	the sample, comparing the level of MN/CA9 gene expression product to		
CC	the average level of MN/CA9 gene expression product in comparable samples		
CC	taken from vertebrates afflicted by the same preneoplastic/neoplastic		
CC	disease as the subject vertebrate, and determining that the subject		
CC	vertebrate has a poorer prognosis if the level of MN/CA9 gene expression		
CC	product quantitated is higher than the average level of MN/CA9 gene		
CC	expression product in the comparable samples. The methods and		
CC	compositions of the present invention are useful in medical genetics, for		
CC	biochemical engineering, immunochemistry and oncology, in particular for		
CC	prognosticating preneoplastic/neoplastic diseases of gastric mucosa,		
CC	gallbladder, biliary ducts, ductal cells of duodenal glands, testis		
CC	including ductular efferens and rete testis, ovary including surface		
CC	coelomic epithelium and rete ovary, basal cells of hair follicles and		
CC	central nervous system choroid plexus. This sequence represents cDNA		
CC	encoding the human MN/CA IX polypeptide of the invention.		
XX			
SQ	Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;		
	Alignment Scores:		
	Pred. No.:	1.85e-130	Length: 1522
	Score:	2424.00	Matches: 459
	Percent Similarity:	100.0%	Conservative: 0
	Best Local Similarity:	100.0%	Mismatches: 0
	Query Match:	100.0%	Indels: 0
	DB:	14	Gaps: 0
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QY	1	MetAlaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProAlaProGly	20
Db	13	ATGGCTCCCTGTGCCACAGCCCTGGCTCCCTCTGTGATCCCGCCCTGCTCCAGGC	72
QY	21	LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu	40
Db	73	CTCAGTGTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	132
QY	41	ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu	60
Db	133	CCCGGATGCAGGAGGATTCCCTTGGGAGGAGGCTCTTCTGGGGAAGATGACCCACTG	192
QY	61	GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu	80
Db	193	GGCGAGGAGGATCTGCCAGTAGAGGATTCACCACAGAGAGAGGATTCACCCGGAGAG	252
QY	81	GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro	100

Db 253 GAGGATCTACCTGGAGGAGGATCTACCTGGAGGAGGATCTACCTGAAGTTAAGCCT 312  
Qy 101 LysSerGluGluGluGlySerLeuLeuGluAspLeuProThrValGluAlaProGly 120  
Db 313 AAATCAGAAAGAGGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTTAGGGCTCTCTGGA 372  
Qy 121 AspProGlnGluProGlnAenAenAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
Db 373 GATCCTCAGAACCCAGATATATCCACAGGACAAAGAGGGATGACACAGATCAT 432  
Qy 141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160  
Db 433 TGGCGCTATGAGGCGACCCGCTGCGCCCGGGTGTCCACAGCTGCGCGGCGCGCTTC 492  
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180  
Db 493 CAGTCCCGGTGATATCCCGCCCGAGCTCGCCGCTTCCTGCGCGGCGCTGCGCCCGCTG 552  
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAenAenGlyHis 200  
Db 553 GAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGNACTGGCGCTCGCGCAATGGCCAC 612  
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220  
Db 613 AGTGTCAACTGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGCTCCCGGGCGGGAGTAC 672  
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTyrGlyAlaAlaGlyVargProGlySerGluHisThr 240  
Db 673 CGGGCTCTGAGCTGATCTGCACTGGGGGGCTGCGAGTGGTCTCGGGCTCGGAGCACACT 732  
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260  
Db 733 GTGGAGGCCACCGTTTCCCTCGGAGATCCAGTGGTTCACCTCAGCACCGCTTTGCC 792  
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280  
Db 793 AGAGTTGACGAGGCTTTGGGGCGCGGGAGGCTGGCGCTGTGGCGGCTTTCTGGAG 852  
Qy 281 GluGlyProGluAenSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300  
Db 853 GAGGGCGCGGAGAAACAGTGCTATGAGCAGTTGCTGCTCGCTTGGAGAAATCGCT 912  
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320  
Db 913 GAGGAGGCTCAGAGACTCAGTCCAGGACTGGACATCTGCACCTCTCGCTCTGAC 972  
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340  
Db 973 TTCAGCGCTACTTCCAAATATGAGGGTCTCTGACTACACCGGCTGTGCGCAGGGTGTG 1032  
Qy 341 IleThrThrValPheAenGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
Db 1033 ATCTGGACTGTGTTTAAACAGACAGTATGCTGAGTGTAAAGCAGCTCCACACCTCTCT 1092  
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAenPheArgAlaThrGlnPro 380  
Db 1093 GACACCTGTGGGACCTGTGACTCTCGGCTACAGTGAATCTCCGAGCAGCGACGCT 1152  
Qy 381 LeuAenGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
Db 1153 TTGAATGGCGAGTGATTTGAGGCTCTTCCCTGCTGGAGTGGACAGCAGTCTCTCGGGCT 1212  
Qy 401 AlaGluProValGlnLeuAenSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
Db 1213 GCTGAGCAGTCCAGCTGGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272  
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440  
Db 1273 GGCTCTCTTTTGTCTGTCACAGGCTCGGTTCTCTGTCAGATGAGAGGAGCAGACA 1332  
Qy 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459  
Db 1333 AGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACTGGAGCC 1389

## RESULT 11

ABL64779  
ID ABL64779 standard; DNA; 1552 BP.  
XX  
AC ABL64779;  
DT 15-MAY-2002 (first entry)  
XX  
DE Lung cancer related gene sequence SEQ ID NO:3116.  
XX  
KW Human; cancer; colon; breast; kidney; thyroid;  
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilms's tumour; adenocarcinoma;  
KW gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200194629-A2.  
XX  
PD 13-DEC-2001.  
XX  
PF 30-MAY-2001; 2001WO-US010838.  
XX  
PR 05-JUN-2000; 2000US-0209473P.  
PR 05-JUN-2000; 2000US-0209531P.  
PR 18-SEP-2000; 2000US-0233133P.  
PR 18-SEP-2000; 2000US-0233617P.  
PR 20-SEP-2000; 2000US-0234009P.  
PR 20-SEP-2000; 2000US-0234034P.  
PR 20-SEP-2000; 2000US-0234052P.  
PR 22-SEP-2000; 2000US-0234509P.  
PR 22-SEP-2000; 2000US-0234567P.  
PR 25-SEP-2000; 2000US-0234923P.  
PR 25-SEP-2000; 2000US-0234924P.  
PR 25-SEP-2000; 2000US-0235077P.  
PR 25-SEP-2000; 2000US-0235082P.  
PR 25-SEP-2000; 2000US-0235134P.  
PR 25-SEP-2000; 2000US-0235280P.  
PR 26-SEP-2000; 2000US-0235637P.  
PR 26-SEP-2000; 2000US-0235638P.  
PR 27-SEP-2000; 2000US-0235711P.  
PR 27-SEP-2000; 2000US-0235720P.  
PR 27-SEP-2000; 2000US-0235840P.  
PR 28-SEP-2000; 2000US-0235863P.  
PR 28-SEP-2000; 2000US-0236028P.  
PR 28-SEP-2000; 2000US-0236032P.  
PR 28-SEP-2000; 2000US-0236033P.  
PR 28-SEP-2000; 2000US-0236034P.  
PR 28-SEP-2000; 2000US-0236109P.  
PR 28-SEP-2000; 2000US-0236111P.  
PR 29-SEP-2000; 2000US-0236842P.  
PR 29-SEP-2000; 2000US-0236891P.  
PR 02-OCT-2000; 2000US-0237172P.  
PR 02-OCT-2000; 2000US-0237173P.  
PR 02-OCT-2000; 2000US-0237278P.  
PR 02-OCT-2000; 2000US-0237294P.  
PR 02-OCT-2000; 2000US-0237295P.  
PR 02-OCT-2000; 2000US-0237316P.  
PR 03-OCT-2000; 2000US-0237425P.  
PR 03-OCT-2000; 2000US-0237598P.  
PR 03-OCT-2000; 2000US-0237604P.  
PR 03-OCT-2000; 2000US-0237606P.  
PR 03-OCT-2000; 2000US-0237608P.  
PR 01-NOV-2000; 2000US-0244867P.  
PR 01-NOV-2000; 2000US-0244868P.  
XX  
XX (AVAL-) AVALON PHARM.  
XX  
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;  
PI Soppet DR, Weaver Z;  
XX  
XX WPI; 2002-188264/24.  
DR

XX Screening for anti-neoplastic agent involves exposing cells to a chemical  
PT agent to be tested for anti-neoplastic activity, and determining a change  
PT in expression of a gene of a signature gene set.

XX Claim 1; SEQ ID NO 3116; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-  
CC neoplastic agent. The method involves exposing cells to a chemical agent  
CC to be tested for anti-neoplastic activity, determining a change in  
CC expression of at least one gene (I) of a signature gene set, where (I)  
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664  
CC to ABL70110), or is at least 95% identical to (S), where a change in  
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic  
CC activity and can be used in gene therapy. M1 can be used for screening an  
CC anti-neoplastic agent, and can be used for producing a product which is  
CC the data collected with respect to the anti-neoplastic agent as a result  
CC of M1, and the data is sufficient to convey the chemical structure and/or  
CC properties of the agent. M1 can be used in the treatment of cancer such  
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,  
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell  
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous  
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's  
CC tumour

XX SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1,88e-130 Length: 1552  
Score: 2424.00 Matches: 459  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0

US-09-967-237B-2 (1-459) x ABL64779 (1-1552)

QY 1 MetAlaProLeuCysProSerProTTPLeuProLeuLeuLeuLeuProAlaProGly 20  
DB 43 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGTGATCCGGCCCTGTCTCCAGGC 102  
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40  
DB 103 CTCACTGTGAACGTGCTGTCTCACTGCTCTGTGATGCTGTCACTCCAGAGGTTG 162  
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60  
DB 163 CCCCGATGAGGAGGATTCCTCCCTGGGAGGAGGCTCTTCTGGGAGATGATGCCACTG 222  
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80  
DB 223 GGGCAGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGATCCACCCGAGAG 282  
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValHisPro 100  
DB 283 GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCT 342  
QY 101 LysSerGluGluGlySerLeuLeuLeuLeuLeuLeuLeuProThrValGluAlaProGly 120  
DB 343 AAATCAGAAGAGAGGCTCCCTGAAGTTAGAGGATCTACTACTGTGGGCTCTCTGGA 402  
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
DB 403 GATCCTCAAGAACCCCAAGATATATGCCACAGGACAAAGAGGGGATGACAGAGTCAT 462  
QY 141 TrpArgTyrGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160  
DB 463 TGGCGCTATGAGCGCAGCCCGCTTGGCCCGGGGTGTCCCGACCGCTGCGCGGCGGCTC 522  
QY 161 GlnSerProValAspLeuLeuArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180  
DB 523 CAGTCCCGGTGATATCCCGCCCCCAGCTGCGGCCCTTCTGCGCGGCCCTTGCGCCCCCTG 582

QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200  
DB 583 GAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTCGCGCTCGCAACATATGGCCAC 642  
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuLeuGlyProGlyArgGluTyr 220  
DB 643 AGTGTGCNACTGACCTTGGCTCTCGGGCTAGAGATGGCTCTGGGTCCCGGCGGAGTAC 702  
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240  
DB 703 CGGGCTCTGCAGCTGCATCTGCACCTGGGGGCTGCAGGTCTCGCGCTCGGAGCACACT 762  
QY 241 ValGluGlyHisArgPheProAlaGluLeuHisValHisLeuSerThrAlaPheAla 260  
DB 763 GTGGAAAGGCCACCTTTCCTCGCGAGATCCAGTGTTCACCTCAGCACCGCTTTGGCC 822  
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280  
DB 823 AGAGTTGACGAGGCTTGGGGCCCGGGAGGCTGCGGTGTGGCGGCTTTCTGGAG 882  
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluAla 300  
DB 883 GAGGGCCCGGAGAGAAACAGTGTCTATGAGCAGTGTGTCTCGCTTGGAGAAATCGCT 942  
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspLeuSerAlaLeuLeuProSerAsp 320  
DB 943 GAGGAAGGCTCAGAGACTCAGGTCCAGGATCGGACATATCTGCATCTCCCTCTCGAC 1002  
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340  
DB 1003 TTCAGCGCTACTTCCANATATGAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGTCTC 1062  
QY 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
DB 1063 ATCTGGACTGTGTTTAACCCAGACAGTGTGCTGAGTGTCTAAGCAGCTCCACACCTCTCT 1122  
QY 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380  
DB 1123 GACACCTCTGGGGAGCTGTGTACTCTCGCTACAGCTGAACTTCCGAGCGAGCGACCT 1182  
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
DB 1183 TTGAATGGGCGAGTGTGAGGCTCTCTCCCTCTGTGGAGTGGAGCAGCAGCTCTCGGGCT 1242  
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
DB 1243 GCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGTGCTGCTGACATCTAGCCTGGTTTTT 1302  
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440  
DB 1303 GGCTCTCTTTTGTCTGTCTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1362  
QY 441 ArgGlyThrIysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyValA 459  
DB 1363 AGGGGAACCAAGGGGTGTGAGCTACCGCCCGCAGCAGAGTACCGAGACTGGAGCC 1419  
RESULT 12  
ABL62179  
ID ABL62179 standard; DNA; 1552 BP.  
XX ABL62179;  
AC ABL62179;  
XX 15-MAY-2002 (first entry)  
DT 15-MAY-2002 (first entry)  
XX Colon adenocarcinoma related gene sequence SEQ ID NO:516.  
DE Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;  
XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;  
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;  
KW gene; ds.  
XX Homo sapiens.  
OS



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Db      823  AGAGTTGACGAGGCTTGGGGGCGCCGGAGGCGCTGGCCGTGTGGCCGCTTTCTGGAG 882
Qy      281  GluGlyProGluGluAenSerAlaTyrGluGluLeuLeuSerArgLeuGluGluIleAla 300
      |||
Db      883  GAGGCGCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTGGGAAGAAATCGCT 942
Qy      301  GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
      |||
Db      943  GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGACATATCTGCATCTCCCTGCCCTCTGAC 1002
Qy      321  PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340
      |||
Db      1003  TTGAGCGCTACTTCCATATGAGGGGTCTTGACTACACCGCCCTGTGCCCAAGGTGTC 1062
Qy      341  IleTrpThrValPheAenGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
      |||
Db      1063  ATCTGGACTGTGTTAAACACAGACAGTGTCTGAGTCTAAGCAGCTCCACACCCCTCTCT 1122
Qy      361  AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAenPheArgAlaThrGlnPro 380
      |||
Db      1123  GACACCCCTGTGGGACCTGGTGAATCTCGGCTACAGCTGAACCTTCCGAGCGACGACCT 1182
Qy      381  LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
      |||
Db      1183  TTGAATGGGCGAGTGATTGAGGCTCTTCCCTGCTGGAGTGGACAGCAGTCTCGGGCT 1242
Qy      401  AlaGluProValGlnLeuAenSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
      |||
Db      1243  GCTGAGCAGCTCCAGCTGAATCTCGCTGGCTGCTGTGACATCTAGCCCTGGTGTCTT 1302
Qy      421  GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgGlnHisArg 440
      |||
Db      1303  GGCTCTCTTTTCTGTGCACAGCGCTGCGGTTCCTTGTGCAGATGAGAAGCGACAGACA 1362
Qy      441  ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
      |||
Db      1363  AGGGGAACCAAGGGGTGTGAGCTACCGCCGACGAGAGTAGCCGAGACTGGAGCC 1419

RESULT 13
ABL65416
ID      ABL65416 standard; DNA; 1552 BP.
XX
AC      ABL65416;
XX
DT      15-MAY-2002 (first entry)
XX
DE      Lung cancer related gene sequence SEQ ID NO:3753.
XX
KW      Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW      stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW      cytostatic; Gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
KW      gene; ds.
XX
OS      Homo sapiens.
XX
PN      WO200194629-A2.
XX
PD      13-DEC-2001.
XX
PF      30-MAY-2001; 2001WO-US010838.
XX
PR      05-JUN-2000; 2000US-0209473P.
PR      05-JUN-2000; 2000US-0209531P.
PR      18-SEP-2000; 2000US-0231333P.
PR      18-SEP-2000; 2000US-0233617P.
PR      20-SEP-2000; 2000US-0234009P.
PR      20-SEP-2000; 2000US-0234034P.
PR      20-SEP-2000; 2000US-0234052P.
PR      22-SEP-2000; 2000US-0234509P.
PR      22-SEP-2000; 2000US-0234567P.
PR      25-SEP-2000; 2000US-0234923P.
PR      25-SEP-2000; 2000US-0234924P.
PR      25-SEP-2000; 2000US-0235077P.
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PR      25-SEP-2000; 2000US-0235082P.
PR      25-SEP-2000; 2000US-0235134P.
PR      25-SEP-2000; 2000US-0235280P.
PR      26-SEP-2000; 2000US-0235637P.
PR      26-SEP-2000; 2000US-0235638P.
PR      27-SEP-2000; 2000US-0235711P.
PR      27-SEP-2000; 2000US-0235720P.
PR      27-SEP-2000; 2000US-0235840P.
PR      27-SEP-2000; 2000US-0235863P.
PR      28-SEP-2000; 2000US-0236028P.
PR      28-SEP-2000; 2000US-0236032P.
PR      28-SEP-2000; 2000US-0236033P.
PR      28-SEP-2000; 2000US-0236034P.
PR      28-SEP-2000; 2000US-0236109P.
PR      28-SEP-2000; 2000US-0236111P.
PR      29-SEP-2000; 2000US-0236842P.
PR      29-SEP-2000; 2000US-0236891P.
PR      02-OCT-2000; 2000US-0237172P.
PR      02-OCT-2000; 2000US-0237173P.
PR      02-OCT-2000; 2000US-0237278P.
PR      02-OCT-2000; 2000US-0237294P.
PR      02-OCT-2000; 2000US-0237295P.
PR      02-OCT-2000; 2000US-0237316P.
PR      03-OCT-2000; 2000US-0237425P.
PR      03-OCT-2000; 2000US-0237598P.
PR      03-OCT-2000; 2000US-0237604P.
PR      03-OCT-2000; 2000US-0237606P.
PR      03-OCT-2000; 2000US-0237608P.
PR      01-NOV-2000; 2000US-0244867P.
PR      01-NOV-2000; 2000US-0245084P.
XX
XX      (AVAL-) AVALON PHARM.
PA
XX      Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI      Soppet DR, Weaver Z;
XX
XX      WPI; 2002-188264/24.
XX
PT      Screening for anti-neoplastic agent involves exposing cells to a chemical
PT      agent to be tested for anti-neoplastic activity, and determining a change
PT      in expression of a gene of a signature gene set.
XX
XX      Claim 1; SEQ ID NO 3753; 44pp; English.
XX
CC      The present invention describes a method (M1) for screening for an anti-
CC      neoplastic agent. The method involves exposing cells to a chemical agent
CC      to be tested for anti-neoplastic activity, determining a change in
CC      expression of at least one gene (I) of a signature gene set, where (I)
CC      comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC      to ABL70110), or is at least 95% identical to (S), where a change in
CC      expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC      activity and can be used in gene therapy. M1 can be used for screening an
CC      anti-neoplastic agent, and can be used for producing a product which is
CC      the data collected with respect to the anti-neoplastic agent as a result
CC      of M1, and the data is sufficient to convey the chemical structure and/or
CC      properties of the agent. M1 can be used in the treatment of cancer such
CC      as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC      prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC      cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC      cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC      tumour
XX
SQ      Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1-88e-130      Length:      1552
Score:          2424.00      Matches:      459
Percent Similarity: 100.0%      Conservatives: 0
Best Local Similarity: 100.0%      Mismatches: 0
Query Match:    100.0%      Indels:      0
DB:            6      Gaps:      0

US-09-967-237B-2 (1-459) x ABL65416 (1-1552)
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Qy	1	MetAlaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProAlaProGly	20
Db	43	ATGGCTCCCTGTGTGCCCGAGCCCTGCCTCCTTGTGTATCCCGGCCCTGTCTCCAGGC	102
Qy	21	LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu	40
Db	103	CTCACTGTGCAACTGTCTGTCTACCTGCTTCTGTATGCTGTTCATTCCCAGAGGTTG	162
Qy	41	ProArgMetGlnGluAspSerProLeuGlyVgLySerSerGlyGluAspAspProLeu	60
Db	163	CCCCGGATGAGGAGGATTTCCCTCTGGGAGGAGCTCTTCTGGGAAGAATGACCCTAG	222
Qy	61	GlycLeuAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu	80
Db	223	GGCGAGGAGGATGTGCCCATGAAGAGATTCACCCAGAGAGGAGGATCCACCGGAGAG	282
Qy	81	GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro	100
Db	283	GAGGATCTACCTGGAGAGGAGTCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCT	342
Qy	101	LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly	120
Db	343	AAATCAGAAGAAGAGGCTCCCTGAAGTTAGAGGATCTACTCTGTTAGGCTCTTGGA	402
Qy	121	AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis	140
Db	403	GATCCTCAAGNACCCCAAGATNTATGCCACAGGGACAAGAGGGGATGACACAGATCAT	462
Qy	141	TrpArgTyrglyGlyAspProProTrpProArgValserProlaCysAlaGlyArgPhe	160
Db	463	TGGCGCTATGGAGGCGACCCGCCCTGCCCGGTGTCCCAGCGCTGCGCGGCGCGCTTC	522
Qy	161	GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu	180
Db	523	CAGTCCCGGTGGATATCCGCCCCACGCTCGCGCCCTTCCTGCCCGGCCCTGCGCCCCCTG	582
Qy	181	GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAnGlyHis	200
Db	583	GAATCTCTGGGCTTCAGCTCCCGCCGCTCCAGNACTGGCGCTGGCCAACATGGCCAC	642
Qy	201	SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyrr	220
Db	643	AGTGTGCAACTGACCCCTGCCTCTCTGGGCTAGAGATGGCTCTGGGTCCCGGGCGGAGTAC	702
Qy	221	ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr	240
Db	703	CGGSGCTTGCACTGTGCATCTGCATCGGGGGGCTGCAGSTGCTCGGGGCTCGGAGCACCT	762
Qy	241	ValGluGlyHisArgPheProAlaGluIleHisValHisLeuSerSerThrAlaPheAla	260
Db	763	GTGGAAGGCCACCGTTTTCTCTGCCGAGATCCACGTGGTTCACTTCAGCACCGGCTTTGCC	822
Qy	261	ArgValAspGluAlaLeuGlyArgProGlyVgLyLeuAlaValLeuAlaPheLeuGlu	280
Db	823	AGAGTTGACGAGGCTTTGGGGGCCCCGGAGGCTTGCCGTGTGGCCGCTTTCTGGAG	882
Qy	281	GluGlyProGluGluAenSerAlaTyrgLuGlnLeuLeuSerArgLeuGluGluIleAla	300
Db	883	GAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTGTGCTGTCTGCTTGGGAAGAAATCGCT	942
Qy	301	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp	320
Db	943	GAGGAAGGCTCAGAGATCTAGGTCCTCCAGGACTGGACATACTGCATCTCTGCCCTCTGAC	1002
Qy	321	PheSerArgTyrrPheGlnTyrglySerLeuThrThrProProCysAlaGlnGlyVal	340
Db	1003	TTACAGCCGCTACTTCCAAATATGAGGGGTCTCTGACTACCGCCCTGTGCCAGGGGTCTC	1062
Qy	341	IleTrpThrValPheAenGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer	360
Db	1063	ATCTGGACTGTGTTTAACGACACAGTGAATGCTGAGTGTCTAAGCAGCTCCACACCCCTCTCT	1122
Db			

Qy	361	AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro	380
Db	1123	GACACCTGTGGGGACCTCTGTGTGACTCTCGGCTACAGCTGAACCTCCGAGCGCAGCCT	1182
Qy	381	LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla	400
Db	1183	TTGAATGGGGGAGTGATTGAGGCTCTCTCCCTGCTGGAGTGGACAGCAGTCTCTGGGCT	1242
Qy	401	AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe	420
Db	1243	GCTGAGCCAGTCCAGCTGAATCTCGCTGGCTGCTGTCACATCTCTAGCCCTGGTTTTT	1302
Qy	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440
Db	1303	GGGCTCTCTTTTGTCTGTCACAGCGTGGCTTCTCTGTGTGAGATGAGAGGCGACACAGA	1362
Qy	441	ArgGlyThrIysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla	459
Db	1363	AGGGGAACCAAGGGGGTGTGAGTACCGCCCAAGAGGTAGCCGAGACTGGAGCC	1419
RESULT 14			
ABL68346			
ID	ABL68346 standard; DNA; 1552 BP.		
XX	XX		
XX	ABL68346;		
XX	XX		
DT	15-MAY-2002 (first entry)		
XX	XX		
DE	Kidney cancer related gene sequence SEQ ID NO:6683.		
XX	XX		
KW	Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;		
KW	stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;		
KW	cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;		
KW	gene; ds.		
OS	Homo sapiens.		
XX	XX		
FN	WO200194629-A2.		
XX	XX		
PD	13-DEC-2001.		
XX	XX		
PF	30-MAY-2001; 2001WO-US010838.		
XX	XX		
PR	05-JUN-2000; 2000US-0209473P.		
PR	05-JUN-2000; 2000US-0209531P.		
PR	18-SEP-2000; 2000US-0233133P.		
PR	18-SEP-2000; 2000US-0233617P.		
PR	20-SEP-2000; 2000US-0234009P.		
PR	20-SEP-2000; 2000US-0234034P.		
PR	20-SEP-2000; 2000US-0234052P.		
PR	22-SEP-2000; 2000US-0234509P.		
PR	22-SEP-2000; 2000US-0234567P.		
PR	25-SEP-2000; 2000US-0234923P.		
PR	25-SEP-2000; 2000US-0234924P.		
PR	25-SEP-2000; 2000US-0235077P.		
PR	25-SEP-2000; 2000US-0235082P.		
PR	25-SEP-2000; 2000US-0235134P.		
PR	25-SEP-2000; 2000US-0235280P.		
PR	26-SEP-2000; 2000US-0235637P.		
PR	26-SEP-2000; 2000US-0235638P.		
PR	27-SEP-2000; 2000US-0235711P.		
PR	27-SEP-2000; 2000US-0235720P.		
PR	27-SEP-2000; 2000US-0235840P.		
PR	27-SEP-2000; 2000US-0235863P.		
PR	28-SEP-2000; 2000US-0236028P.		
PR	28-SEP-2000; 2000US-0236032P.		
PR	28-SEP-2000; 2000US-0236033P.		
PR	28-SEP-2000; 2000US-0236034P.		
PR	28-SEP-2000; 2000US-0236109P.		
PR	28-SEP-2000; 2000US-0236111P.		
PR	29-SEP-2000; 2000US-0236842P.		
PR	29-SEP-2000; 2000US-0236891P.		
PR	02-OCT-2000; 2000US-0237172P.		

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PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
PI
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 6683; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 847 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
CC tumour.
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

```

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Alignment Scores:
Pred. No.: 1-88e-130 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 6 Gaps: 0

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US-09-967-237B-2 (1-459) x ABL68346 (1-1552)

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QY 1 MetaProLeuCysProSerProTrpLeuProLeuLeuLeuProAlaProGly 20
DB 43 ATGGCTCCCTGTGGCCAGCCCTGGCTCCCTCTGTTCATCCGCGCCCTGCTCCAGGC 102
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 103 CTCACTGTGCAACTGTGCTGTCTCACTGCTGCTTCTGTATGCTCTCATCCCGAGAGGTG 162
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
DB 163 CCCCGGATGAGAGGAGGATCCCTCTGGAGGAGGCTCTCTCGGGAAGATGATCCCACTG 222
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
DB 223 GGGCAGGAGGATGCGCCAGTGAAGAGGATTCACCCAGAGAGGAGGATCCACCCCGGAGAG 282
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100

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DB 283 GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAAGTTAAGCCT 342
QY 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
DB 343 AAATCAGAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTGAGGCTCTCTGGA 402
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
DB 403 GATCTCTCAAGAACCCCAAGTAATGCCACAGGGGCAAAAGAGGGGATACCCAGAGTCAAT 462
QY 141 TrpArgTyrGlyGlyAspProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
DB 463 TGGCGCTATGGAGGAGACCCCGCCCTGGCCCGGGTGTCCCGAGCCTGCGCGGGCCGCTTC 522
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB 523 CAGTCCCGGTGGATATCCGCCCGCCAGCTCGCGCGCTTCTGCGCGCCCTCGCGCCCTG 582
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlnHis 200
DB 583 GAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTCGCGCTGCGCAACAATGGCCAC 642
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
DB 643 AGTGTGCAACTGACCCCTGCTCTGGGCTAGAGATGGCTCTGGGTCCCGGGCGGAGTAC 702
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240
DB 703 CGGGCTCTCGAGCTGCATCTGCACCTGGGGGGCTCGAGGTCGTCCGGCTCGGAGCACACT 762
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
DB 763 GTGGAAGGCCACCGTTCCTCCCGAGATCCACGTGGTTCACCTCAGCACCCGCTTTGCC 822
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
DB 823 AGAGTTGACAGGCTCTGGGGGGCCCGGAGGCTGGCCGTGTGGCCGCTTTCTGGAG 882
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluLeuAla 300
DB 883 GAGGGCCCGGAAGAAAACAGTGCCTATGAGCAGTGTGCTGCTCGCTTGAAGAAATCGCT 942
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
DB 943 GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCCTCTCGCCCTCTGAC 1002
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340
DB 1003 TTCAGCGGCTACTTCCATATGAGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGTG 1062
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
DB 1063 ATCTGGACTGTGTTAAACCAAGCAGTGTGCTGAGTGTCTAAGCAGCTCCACACCCCTCT 1122
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
DB 1123 GACACCCCTGTGGGACCTCGTGACTCTCGGCTACAGCTGAATCTCCGAGCAGCAGCCT 1182
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
DB 1183 TTGAATGGCGAGTGTGATGGGCTCTCTCCCTGTGGAGTGGAGCAGCAGTCTCTCGGGCT 1242
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
DB 1243 GCTGAGCCAGTCCAGCTGAATTCCTGCTGGCTGTGCTGTGACATCTAGACCCCTGGTTTTT 1302
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgGlnHisArg 440
DB 1303 GGCCTCTCTTTTGTGCTGTCACCGCGTCCGCTTCTTGTGATGAGAGGAGCAGACAGA 1362
QY 441 ArgGlyThrLysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459

```





```
Qy      341  IleTTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
Db      1063  ATCTGGACTGTGTTTAACACAGACAGTGATGCTGAGTGCTAAGCAGGCTCCACACCCCTCTCT 1122

Qy      361  AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db      1123  GACACCCCTGTGGGACCTGTGTGACTCTCGGCTACAGCTGAACCTCCGAGCGACGACGCT 1182

Qy      381  LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db      1183  TTGAATGGGCGAGTGATTGAGGCTCTCTCCCTGCTGGAGTGGACAGAGTCCTCGGGCT 1242

Qy      401  AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db      1243  GCTGAGCCAGTCCAGCTGAATTCTGTGCTGGCTGGTGCATCTAGCCCTGGTTTTT 1302

Qy      421  GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db      1303  GGCCTCCTTTTGTGTACCGCGTGGCGTTCTTGTGCAGATGAGAAGGCACACAGA 1362

Qy      441  ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db      1363  AGGGGAACCAAGGGGGTGTGAGCTACCGCCACGACGAGGTAGCCGAGACTGGAGCC 1419
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Search completed: February 17, 2006, 14:47:57

Job time : 864 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 17, 2006, 14:48:07 ; Search time 5571 Seconds  
(without alignments)

3854.832 Million cell updates/sec

Title: US-09-967-237B-2

Perfect score: 2424

Sequence: 1 MAPLCFSPWLPPLIPAPAGP.....RRGTGKGVSRPAEVAETGA 459

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSWEB.spool/US09967237/runat\_15022006.182244\_28001/app\_query.fasta\_1  
-DB=EST -OPMT=fastap -SUFFIX=ret -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOALIGN=200 -THR\_SCORE=pcr -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs03h  
-USER=US09967237 @CGN 1.1.5315 @runat\_15022006.182244\_28001 -NCPU=6 -ICPU=3  
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2420	99.8	1469	4	CR616345 full-leng
2	2420	99.8	1523	4	CR620502 full-leng
3	2420	99.8	1541	4	CR597234 full-leng
4	2361.5	97.4	1492	4	CR590646 full-leng
5	2177	89.8	1380	11	DQ049266 Homo sapi
6	1926	79.5	1380	11	DQ049267 Pan trogl
7	1790	73.8	1084	1	AL542336

8	1567	64.6	1070	1	AL554705	AL554705
9	1556.5	64.2	1009	1	AL558378	AL558378
10	1501.5	61.9	1017	5	AX401186	AX401186
11	1472	60.7	916	5	AX423970	AX423970
12	1452.5	59.9	971	7	CO579387	CO579387
13	1401	57.8	927	1	AL555184	AL555184
14	1370	56.5	830	8	DR432523	DR432523
15	1360	56.1	887	1	AJ924825	AJ924825
16	1332	55.0	1071	1	AL554665	AL554665
17	1319	54.4	833	8	DR432759	DR432759
18	1304.5	53.8	874	2	EG386425	EG386425
19	1289.5	53.2	815	8	DR432519	DR432519
20	1260	52.0	811	8	DR432758	DR432758
21	1223	50.5	693	8	DR433331	DR433331
22	1211	50.0	836	5	AX383092	AX383092
23	1160	47.9	692	8	DR432847	DR432847
24	1130	46.6	740	7	CK971835	CK971835
25	1122.5	46.3	687	8	DR432755	DR432755
26	1121	46.2	675	8	DR432851	DR432851
27	1121	46.2	1017	1	AL580216	AL580216
28	1115	46.0	994	1	AL577748	AL577748
29	1114	46.0	668	2	BG824243	BG824243
30	1113	45.9	818	2	BE548062	BE548062
31	1094	45.1	975	1	AJ924826	AJ924826
32	1092	45.0	782	7	CK969500	CK969500
33	1090	45.0	961	5	AX423969	AX423969
34	1075	44.3	722	7	CK978804	CK978804
35	1064.5	43.9	746	2	BI223232	BI223232
36	1060.5	43.8	806	2	BF344769	BF344769
37	1041	42.9	589	3	BM790508	BM790508
38	1041	42.9	813	7	CO734371	CO734371
39	1007.5	41.6	962	7	CV675676	CV675676
40	1003	41.4	663	8	DR432756	DR432756
41	1002.5	41.4	736	2	BE543633	BE543633
42	998.5	41.2	666	8	DR433328	DR433328
43	989	40.8	830	7	CK849799	CK849799
44	986.5	40.7	945	6	CF579370	CF579370
45	965	39.8	715	7	CK963805	CK963805

#### ALIGNMENTS

RESULT 1	CR616345	1469 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CS0DA003YB12 of Neuroblastoma of Homo sapiens (human).				
DEFINITION	CR616345				
ACCESSION	CR616345.1	GI:50497152			
VERSION	HTC; CNSLT cdna				
KEYWORDS	Homo sapiens				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1469)				
AUTHORS	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2 (bases 1 to 1469)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)				
COMMENT	- Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime ends enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.				

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FEATURES
  source
    Location/Qualifiers
      1. 1469
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="CS0A0037B12"
        /issue_type="Neuroblastoma"
        /plasmid="pCMVSPORT_6"

ORIGIN

Alignment Scores:
Pred. No.:      2,92e-185      Length:      1469
Score:          2420.00        Matches:      458
Percent Similarity: 100.0%      Conservative: 1
Best Local Similarity: 99.8%      Mismatches: 0
Query Match:      99.8%        Indels:      0
DB:               4           Gaps:       0

US-09-967-237B-2 (1-459) x CR616345 (1-1469)

QY 1 MetAlaProLeuCysProSerProTrrpLeuProLeuLeuileProAlaProGly 20
DB 5 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTTGATCCGGCCCTGTCCAGGC 64
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 65 CTCACCTGTGCACTGTGCTGTCTCACTGTCTGCTCTTCTGTGTCCTGTCCATCCCCAGAGGTTG 124
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu 60
DB 125 CCCCGGATGCAGAGGAGTCCCCCTTGGAGGAGGCTCTTCTGGGAAGATGACCCACTG 184
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
DB 185 GCGCAGGAGGATGTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGATCCACCCGGAGAG 244
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValHisPro 100
DB 245 GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCT 304
QY 101 LysSerGluGluGlySerLeuLeuLeuLeuLeuLeuLeuProThrValGluAlaProGly 120
DB 305 AAATCAGAAAGAGGCTCCCTGGAAGTTAGAGATCTACTACTGTGTAGGCTCTCTGGA 364
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlyAspAspGlnSerHis 140
DB 365 GATCCTCAAGACCCAGATATATGCCACAGGACAAAGAGGAGTACACAGAGTCAT 424
QY 141 TrpArgTyrGlyGlyAspProProTrrpProArgValSerProAlaCysAlaGlyArgPhe 160
DB 425 TGGCGCTATGGAGCGCACCCCGCTTGGCCCGGGTGTCCCCAGCCTGCGCGGCGCGCTTC 484
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB 485 CAGTCCCGGTGGATATCCCGCCCCAGCTCGCCGCTTCTGCGCGGCTTCCCGCCCCCTG 544
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAnglyHis 200
DB 545 GAATCTCTGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTGCGCAACATGGCCAC 604
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
DB 605 AGTGTGCACTGACCTGCTCTCTGGGTAGAGATGCTGCTGGGTCCCGGCGCGGAGTAC 664
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrrpGlyValaAlaGlyArgProGlySerGluHisThr 240
DB 665 CGGCTCTGCACTGCACTGCACTGCGGGGCTGCAGTCTGCTCGGGCTCGAGACACT 724
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260
DB 725 GTGGAGGCCACCGTTTCCCTGCGGAGATCCAGTGTGTTCACTCCTCAGCACCGCTTTGCC 784
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280

785 AGAGTTGACAGAGCCCTTGGGGCGCCCGGAGGCGCTGCGCGTGTGTGCCCGCTTCTGGAG 844
281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
845 GAGGGCCCGAGAGAAACAGTGCCTATGAGCAGTGTCTGTCTGCTTGGAGAAATCGCT 904
301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
905 GAGGAAGGCTCAGAGACTCAGGTCCCGAGACTGGACATATCTGCATCTCCTGCCCTCTGAC 964
321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
965 TTGAGCCGCTACTTCCATATGAGGGGTCTCTGACTACACCGCCCTGTGCCCCAGGGTGC 1024
341 IleTrrpValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
1025 ATCTGACCTGTGTTTAAACCCAGACAGTGTGCTGAGTGTCTAAGCAGCTCCACACCTCTCT 1084
361 AspThrLeuTrrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
1085 GACACCCCTGTGGGACCTGTGCTACTCTCGCTACAGCTGAACCTTCGAGCGACGACGCT 1144
381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
1145 TTGAATGGCGGAGTGAATTGAGGCTCTCTCCCTGCTGGAGTGGACAGCTCTCCGGCT 1204
401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
1205 GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
1265 GGCTCTCTTTTCTGCTGTCCAGCGCTGCGCTTCTTGTGTCAGATGAGAAGCGACAGAGA 1324
441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
1325 AGGGGAACCAAAAGGGGTGTGAGTACCCGCCAGCAGAGGTAGCCGAGACTGGAGCC 1381

RESULT 2
LOCUS CR620502 1523 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DR007YK10 of HeLa cells Cot 25-normalized
of Homo sapiens (human) .
ACCESSION CR620502
VERSION CR620502.1 GI:50501309
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1523)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1523)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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    Location/Qualifiers
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## ORIGIN

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 Score: 2420.00 Matches: 458  
 Percent Similarity: 100.0% Conservative: 1  
 Best Local Similarity: 99.8% Mismatches: 0  
 Query Match: 99.8% Indels: 0  
 DB: 4 Gaps: 0

US-09-967-237B-2 (1-459) x CR620502 (1-1523)

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 Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40  
 Db 92 CTCACTGTCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 151  
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 Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80  
 Db 212 GCGAGAGGATCTGCCCATGAGAGGATTCACCCAGAGAGGAGATCCACCCGAGAG 271  
 Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100  
 Db 272 GAGGATCTACTGAGAGGAGGATCTACTCTGGAGAGGAGGATCTACTGAGGATTAAGCCT 331  
 Qy 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120  
 Db 332 AAATCAGAAGAAGAGGCTCCCTCAAGTTAGAGATCTACTGTTGAGGCTCTCTGGA 391  
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 DEFINITION of Homo sapiens (human).  
 ACCESSION CR597234  
 VERSION CR597234.1 GI:50478041  
 KEYWORDS HTC; CDSLT cDNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1541)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished  
 REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600  
 Paraday Avenue  
 REFERENCE 2 (bases 1 to 1541)  
 Genoscope.  
 DIRECT SUBMISSION  
 TITLE Direct Submission  
 JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :  
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
 COMMENT - Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life technologies, a  
 division of Invitrogen.  
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## ORIGIN

## Alignment Scores:

Pred. No.: 3,12e-185 Length: 1541  
Score: 2420.00 Matches: 458  
Percent Similarity: 100.0% Conservative: 1  
Best Local Similarity: 99.8% Mismatches: 0  
Query Match: 99.8% Indels: 0  
DB: 4 Gaps: 0

US-09-967-237B-2 (1-459) x CRS97234 (1-1541)

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DB 102 CTCACTGTGCAACTGCTGCTGTCTCACTGCTGCTTCTGCTGCTGTCCATCCCGAGGTTG 161
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
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QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
DB 222 GCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGATCCACCCGAGAG 281
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QY 101 LysSerGluGluGlySerLeuLeuLeuGluAspLeuProThrValGluAlaProGly 120
DB 342 AAATCAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTTGAGGCTCTCTGGA 401
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QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluAla 300
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DB 1302 GGCCTCTTTTGTCTCCACAGCGTCCGCTTCTTTGTGCAGATGAGAAGGACAGCAGA 1361
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DB 1362 AGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGTACCGAGACTGGAGCC 1418
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LOCUS full-length cDNA clone CS0DJ005YK14 of T cells (Jurkat cell line)
DEFINITION Cot 10-normalized of Homo sapiens (human).
ACCESSION CRS90646
VERSION CRS90646.1 GI:50471453
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 1492)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 1492)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
into the Not I and EcoR V sites of the PCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES Location/Qualifiers
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 DB: 4 Gaps: 1

US-09-967-237B-2 (1-459) x CR590646 (1-1492)

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 DB 283 GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAGCCT 342  
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 DB 343 AAATCAGAAGAAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTGGAGGCTCTCGGA 402  
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 DEFINITION Genomic survey sequence.  
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 VERSION DQ049266.1 GI:66902465  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 1380)  
 AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
 Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeillo,D.,  
 White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE A Scan for Positively Selected Genes in the Genomes of Humans and  
 Chimpanzees  
 JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)  
 PUBMED 15869325  
 REFERENCE 2 (bases 1 to 1380)  
 AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,  
 Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civeillo,D.,  
 White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
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US-09-967-237B-2 (1-459) x DQ049266 (1-1380)																			
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Qy	241	ValGluGlyHisArgPheProAlaGluLleHisValValHisLeuSerThrAlaPheAla	260																
Db	721	GTGGAAGGCCACCGTTTCCCTGCCGAGATCCAGCTGGTTCACCTCAGCACCGCCTTTGCC	780																
Qy	261	ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu	280																
Db	781	AGAGTTGACAGGCTTGGGGCGCCCGGAGGCTGCGCGTGTGGCGGCTTCTCTGGAG	840																
Qy	281	GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluLleAla	300																
Db	841	GAGGCGCCGGAAGAAAACAGTGTCTATGACAGATGTGCTGTCTCGCTTGGAGAAATCGCT	900																
Qy	301	GluGluGlySerGluThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp	320																
Db	901	GAGGAAGGCTCAGAGACTCAGTCCAGGACTGGACATATCTGCATCTCTGCCCTCTGAC	960																
Qy	321	PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal	340																
Db	961	TTTCAGCCGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGT	1020																
Qy	341	IleTTPThrValPheAenGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer	360																
Db	1021	ATCTGACTGTGTTTAAACCAGACAGTGATGCTGAGTGCTAAGCAGCTCCACACCTCTCT	1080																
Qy	361	AspThrLeuTTPdlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro	380																
Db	1081	GACACCTCTGGGACCTGTGTGACTCTCGGCTACAGCTGAACCTTCGAGCGACGACGCT	1140																
Qy	381	LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla	400																
Db	1141	TTGAATGGCGAGTGATTGAGGCTCTTCCCTGCTGAGTGCACATCTTAGCCCTGGTTTT	1200																
Qy	401	AlaGluProValGlnLeuAenSerCysLeuAlaAlaGlyAspLysLeuAlaLeuValPhe	420																
Db	1201	GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGGCTGGTGACATCTTAGCCCTGGTTTT	1260																
Qy	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440																
Db	1261	GGCTCTCTTTTGTCTCACAGGCTCGGCTTCTTGTGAGATGAGAAGGCAGCACAGA	1320																
Qy	441	ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla	459																
Db	1321	AGGGGAACCAAGGGGCTGTGAGTACCGCCAGCAGAGGTAGCCGAGACTGGAGCC	1377																
RESULT 6																			
DQ049267	1380 bp	DNA	linear	GSS	02-JUN-2005														
Pan troglodytes CA9 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.																			
LOCUS	DQ049267	1	GI:66902466																
DEFINITION	DQ049267.1	GSS.	Pan troglodytes (chimpanzee)																
ACCESSION	DQ049267																		
VERSION	DQ049267.1																		
KEYWORDS	Pan troglodytes																		
SOURCE	Pan troglodytes																		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Pan.																		
REFERENCE	1 (bases 1 to 1380)																		
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Gnanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.																		
TITLE	A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees																		
JOURNAL	(er) PLoS Biol. 3 (6), E170 (2005)																		
PUBMED	15869325																		
REFERENCE	2 (bases 1 to 1380)																		
AUTHORS	Nielsen,R., Bustamante,C., Clark,A.G., Gnanowski,S., Sackton,T.B., Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.																		
TITLE	Direct Submission																		
JOURNAL	Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA																		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.																		
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ORIGIN																			
Alignment Scores:	2.68e-145	Length:	1380																
Pred. No.:	1926.00	Matches:	385																



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Score: 1790.00 Matches: 337
Percent Similarity: 98.0% Conservative: 4
Best Local Similarity: 96.8% Mismatches: 6
Query Match: 73.8% Indels: 1
DB: 1 Gaps: 0

US-09-967-237B-2 (1-459) x AL542336 (1-1084)

Qy 3 ProLeuCysProSerProTTPLeuProLeuLeuLeuLeuProAlaProAlaProGlyLeuThr 22
Db 29 CCCCTGCGCCCGAGCCCTCGCTCCCTCTGTTGATCCCGGCCCTGCTCCAGGCTCACT 88
Qy 23 ValGlnLeuLeuLeuSerLeuLeuLeuLeuLeuMetProValHisProGlnArgLeuProArg 42
Db 89 GTGCAACTGCTGCTGCTCACTGCTGCTTCTGCTGCTGCTCCATCCCCAGAGGTTGCCCGG 148
Qy 43 MetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeuGlyGlu 62
Db 149 ATGAGGAGGATTCCCTTGGGAGGAGGCTCTTCTGGGGAAGATGATGATCCCTGAGGCGAG 208
Qy 63 GluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGluGluAsp 82
Db 209 GAGGATCTGCCAGTGAAGGATTCCACCCAGAGAGGATCCACCCGAGAGGAGGAT 268
Qy 83 LeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysProLysSer 102
Db 269 CTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCTAAATCA 328
Qy 103 GluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGlyAspPro 122
Db 329 GAAGAAGAGGCTCCCTGGAAGTTAGAGGATCTACTACTGTGAGGCTCTTGAGATCCT 388
Qy 123 GlnGluProGlnAenAenAlaHisArgAspLysGluGlyAspAspGlnSerHisTrpArg 142
Db 389 CAGNACCCCAATATATGCCACAGGACAAAGAGGGGATGACACAGATCATTTGGCGC 448
Qy 143 TyrGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPheGlnSer 162
Db 449 TATGAGGCGCAGCCGCTGCGCCCGGCTGCTCCACGCTGCGCGGCGCGCTTCCAGTCC 508
Qy 163 ProValAspLeuArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeuGluLeu 182
Db 509 CCGGTGGATATCGCCGCCACAGCTGCGCCCTTCTGCGCGGCGCTGCGCCCTGGAATC 568
Qy 183 LeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAenAenGlyHisSerVal 202
Db 569 CTGGGCTTCCAGCTCCCGCGCGCTCCCAAGACTGGCGCTGGCAACATGSCCAGCTGTG 628
Qy 203 GlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyrArgAla 222
Db 629 CAACTGACCTGCTCTGGGCTAGAGATGGCTCTGGGCTCCCGGCGGAGTACCGGGCT 688
Qy 223 LeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThrValGlu 242
Db 689 CTGCAGCTGATCTGCACTGGGGGCTGCGAGGCTGCTCGGGCTCGGAGCACTGTGGAA 748
Qy 243 GlyHisArgPheProAlaGluLeuHisValValHisLeuSerThrAlaPheAlaArgVal 262
Db 749 GGCTACCGTTCCTGCGGAGATCCAGTGGTTCACCTCAGCACCGGCTTTGGCAGAGTT 808
Qy 263 AspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGluGly 282
Db 809 GACGAGGCTTGGGGCGCCGGAGGCTGCGCGCTGTTGGCGCTTCTGAGAGGAGGC 868
Qy 283 ProGluGluAenSerAlaTyrGluGlnLeuLeuSerArgLeuGluLeuAlaGluGlu 302
Db 869 CCGGAAGAAACAGTGCCTATGAGCAGTGTGCTGCTGCTGCTTGGGAAGAAATCGCTGAGAA 928
Qy 303 GlySerGluThrGlnValProGly-LeuAspIleSerAlaLeuLeuProSerAspPheSe 322
Db 929 GGCTCAGAGACTCAGGTCCTCCAGGACTTGGACATATCTKSACTCTGSCCTCTGACTTCAG 988
Qy 322 rArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyValIleTr 342
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Db 989 CCGCTACTTCAATATGAGGGGCTCTGACTACACCGCCCTGTGCGAGGCTGTCATCTK 1048
Qy 342 pThrValPheAsnGlnThrVal 349
Db 1049 GACTGTGTTTAAACAGAMAGTK 1070

RESULT 8
AL554705
LOCUS
DEFINITION
AL554705 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1085YF18 5-PRIME, mRNA sequence.
ACCESSION
VERSION
AL554705.3 GI:45859455
KEYWORDS
SOURCE
EST.
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 1070)
Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31276515.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5300.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0D1085DC090P1&e=5300.f.
FEATURES
Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:9606"
/clone="CS0D1085YF18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.: 2-2e-116 Length: 1070
Score: 1567.00 Matches: 318
Percent Similarity: 92.5% Conservative: 4
Best Local Similarity: 91.4% Mismatches: 22
Query Match: 64.6% Indels: 8
DB: 1 Gaps: 2

US-09-967-237B-2 (1-459) x AL554705 (1-1070)

Qy 1 MetAlaProLeuCysProSerProTTPLeuProLeuLeuLeuProAlaProAlaProGly 20
Db 42 ATGGCTCCCCCTGTGCGCCAGCCCTGCTCCCTCTGTTGATCCCGGCCCTGCTCCAGGC 101
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 102 CTCACTGTGCAACTGCTGCTGCTCACTGCTGCTTCTGCTGCTGCTCATCCCGAGGTTG 161
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu 60
Db 162 CCGCGGATGACAGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAAGATGATGCCACTG 221
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Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
Db 222 GCGGAGGAGGATCGCCAGTGAAGAGATTACCCAGAGAGGAGGATCCACCGGAGAG 281
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
Db 282 GAGGATCTACTGAGAGGAGGATCTACTGAGAGGAGGATCTACTGAAAGTAAAGCCT 341
Qy 101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 342 AAATCAGAAGAAGAGGCTCCCTGAAGTTAGAGATCTACTGTTGAGGCTCTCGGA 401
Qy 121 AspProGluGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
Db 402 GATCTCTAGAACCCAGATATATGCCACAGGACAAAGAGGGGATGACAGATCAT 461
Qy 141 TrpArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 462 TGGCGCTATGAGCGGACCGCCCTGGCCCGGGGTGCCAGGCTCGCGGGCGCGCTTC 521
Qy 161 GlnSerProValAspLysLeuGluGluGluGluGluGluGluGluGluGluGluGlu 180
Db 522 CAGTCCCGGCTGGATATCCGCGCCCTGCGCGCCCTTCTGCGCGCCCTGCGCGCCCTG 581
Qy 181 GluLeuGluGlyPheGlnLeuProProGluLeuArgLeuArgAsnGlyHis 200
Db 582 GAATCTCTGGGCTTCCAGCTCCCGCCCTCCAGACTGGCGCTGCGCTGCGCAATGCGCAC 641
Qy 201 SerValGlnLeuThrLeuProProGlyGluGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 642 AGTGTGCACTGACCTTCCCTGCGGCTAGAGATGCTGCGGCTCCCGGGCGGAGTMC 701
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTyr-GlyAlaAlaGlyArgProGlySerGluHisTh 240
Db 702 CGGCTCTGCACTGCACTCTGCACTGGGGGGGCTGCACTGCTCGCGGCTCGGAGCAC 761
Qy 240 rValGluGlyHisArgPheProAlaGluHisValHisValHisLeuSerThrAlaPheAl 260
Db 762 TGTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGTGGTTTCACTCAGCAGCGCTTTC 821
Qy 260 aArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuG1 280
Db 822 CAGAGTTGACGAGGCTTGGGGCCCGSGGAGGCTGCGCGTGTGGCGGCTTCTTGA 881
Qy 280 uGluGlyProGluGluSerAlaTyrGluGlnLeuLeuSerArgLeuGluLysAl 300
Db 882 GGA-GGGCCGGRAGAAACAGTGCCTATGAGCAGTTCGCTGCTTGGAGAAATCGC 940
Qy 300 aGluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAs 320
Db 941 TGAGGAAGC-TCAGAGACTVAGGKYCCAGGAGCTGGACAAATCTGCATCTGSC--TCTGA 997
Qy 320 pPheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVa 340
Db 998 CTTTCAGCGCT---NWTTCCAWAGAGGCTCTCAT-WMACCGCCCTKTCGAGG----- 1048
Qy 340 lileTyrThrValPheAsnGln 347
Db 1049 -GTTATCTGATTTTWTWACAG 1069

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RESULT 9
AL558378 1009 bp mRNA linear EST 02-APR-2004
LOCUS
DEFINITION AL558378 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
Homo sapiens cdna clone CS0DJ005YK14 5-PRIME, mRNA sequence.
ACCESSION
VERSION AL558378.3 GI:46183776
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.

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# REFERENCE AUTHORS TITLE JOURNAL COMMENT

1 (bases 1 to 1009)  
 Li, W.B., Gruber, C., Jesse, J. and Polayes, D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 On Feb 15, 2001 this sequence version replaced gi:31280177.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-strand cDNA was digested with Not I and cloned  
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
 was normalized. Library was constructed by Life Technologies, a  
 division of Invitrogen. This sequence belongs to sequence cluster  
 5300.f  
 For more information about this cluster, see  
 http://www.genoscope.cns.fr/cdna?S=CS0DJ005BF07QP1&c=5300.f.

## FEATURES

### source

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 /mol\_type="mRNA"  
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 /cell\_line="JURKAT"  
 /clone\_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"  
 /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Alignment Scores:  
 Pred. No.: 1,44e-115 Length: 1009  
 Score: 1556.50 Matches: 311  
 Percent Similarity: 97.8% Conservative: 0  
 Best Local Similarity: 97.8% Mismatches: 7  
 Query Match: 64.2% Indels: 5  
 DB: 1 Gaps: 0  
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 Qy 1 MetAlaProLeuGluCysProSerProTyrLeuProLeuLeuLeuProAlaProGly 20  
 Db 43 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTTGATCCGCGCCCTGTCTCCAGGC 102  
 Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40  
 Db 103 CTCACGTGTCACTGTCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 162  
 Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60  
 Db 163 CCCCAGATGAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGAGAGATGACCCACTG 222  
 Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80  
 Db 223 GCGAGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGATTCACCCGAGAG 282  
 Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100  
 Db 283 GAGGATCTACTGAGAGGAGGATCTACTGAGAGGAGGATCTACTGAGGATTAAGCCT 342  
 Qy 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120  
 Db 343 AAATCAGAAGAAGAGGCTCCCTGAAGTTAGAGATCTACTGTTGAGGCTCTCGGA 402  
 Qy 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
 Db 403 GATCTCTAGAACCCAGATATATGCCACAGGACAAAGAGGGGATGACAGATCAT 462  
 Qy 141 TrpArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160

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Db 463 TGGCGCTATGAGGCGACCGCCTCGCCCGGGTGTCCAGCGCTGCGCGCGCGCTTC 522
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAalPheCysProAlaLeuArgProLeu 180
Db 523 CAGTCCCGGTGGATATCCGCCCGCCAGCTCGCGCGCTTCTGCGCGCGCTGCGCGCGCTG 582
Qy 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAenAnGlyHis 200
Db 583 GAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTCGCGCTGCGCAACAATGGCCAC 642
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 643 AGTGTGCAACTGACCTTCCTCTGGGCTAGAGATGGCTCTGGGTCCCGGCGGAGTAC 702
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTTPGlyAlaAalGlyArgProGlySerGluHisThr 240
Db 703 CGGGCTCTGCAGCTGCATCTGCATCTGGGGGCTGCAGGTGCTCGGGCTCGAGGACACT 762
Qy 241 ValGlnGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGTGGTTTCACTCAGCACCGCTTTGCC 822
Qy 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu 280
Db 823 AGATTGACGAGGCTTGGGGCGCCCGGGAGGCTGGCCGTGTGGC-GCCTTCTGGAG 881
Qy 281 GlnGlyProGlnGluAenSerAlaTyrGlnLeuLeuSerArgLeuGluGluIleAla 300
Db 882 GAGGSCCGGAAGA-AACAGTGCCTATGACAGTGTGCTGCTCGCTTGGGAARA-ATCGCT 939
Qy 301 GlnGluGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuPro 318
Db 940 GAGGAAGC-TCAGAGACTCAGKCCCAGGACTGACAAWATT-GCACTCTCGCT 991

RESULT 10
BX401186
LOCUS
DEFINITION
  BX401186 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
  cDNA clone CS0DK009YP10 5-PRIME, mRNA sequence.
ACCESSION
  BX401186
VERSION
  BX401186.2 GI:46876709
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homiidae; Homo.
REFERENCE
  1 (bases 1 to 1017)
  Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
  On May 13, 2003 this sequence version replaced gi:30626393.
CONTACT
  Genoscope
  Genoscope - Centre National de Sequencage
  2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen. This sequence belongs to sequence cluster
  5300.f
  For more information about this cluster, see
  http://www.genoscope.cns.fr/cdna?s=CS0DK009DH05QP1&c=5300.f.
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/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
Alignment Scores:
Pred. No.: 4,13e-111 Length: 1017
Score: 1501.50 Matches: 290
Percent Similarity: 93.0% Conservatives: 2
Best Local Similarity: 92.4% Mismatches: 19
Query Match: 61.9% Indels: 4
DB: 5 Gaps: 3
US-09-967-237B-2 (1-459) x BX401186 (1-1017)
Qy 3 ProLeuCyProSerProTrpLeuProLeuLeuLeuProAlaProAlaProGlyLeuThr 22
Db 19 CCCTCTGCCCCCAGCCCTGGCTCCCTCTGTGTATCCCGGCCCTCTCCAGGCTCACT 78
Qy 23 ValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeuProArg 42
Db 79 GTGCAACTGCTGTGTCACTGTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 138
Qy 43 MetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeuGlyGlu 62
Db 139 ATGCAGAGGATTTCCCTTTGGGAGGAGGCTCTTTCTGGGAGAGATGACCCACTTGGGCGAG 138
Qy 63 GluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGluGluAsp 82
Db 199 GAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGAGGATCCACCCGAGAGGAGGAT 258
Qy 83 LeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysProLysSer 102
Db 259 CTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCTTAATCA 318
Qy 103 GluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGlyAspPro 122
Db 319 GAAGAAGAGGCTCTCTGAAGTTAGAGGATCTACCTACTGTGTGAGGCTCTCTGAGATCT 378
Qy 123 GlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHisTrpArg 142
Db 379 CAAGAACCCCGAATAATGCCACAGGAGCAAGAAGAGGAGTGCACAGAGTCACTTGGCGC 438
Qy 143 TyrGlyGlyAspProTrpProArgValSerProAlaCysAlaGlyArgPheGlnSer 162
Db 439 TATGGAGGCGACCCCGCTGGCCCGGGGTGTCCCGAGCTGCGCGCGCTTCCAGTCC 498
Qy 163 ProValAspIleArgProGlnLeuAlaAalPheCysProAlaLeuArgProLeuGluLeu 182
Db 499 CCGGTGGATATCCGCCCGCCAGCTCGCGCGCTTCTGCCCGCGCTGCGCGCTTGGAACTC 558
Qy 183 LeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAnGlyHisSerVal 202
Db 559 CTGGGCTTCCAGCTCCCGCGCTCCCGAGAACTGCGCTCGCAACAATGGCCACAGTGTG 618
Qy 203 GlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyrArgAla 222
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Qy 223 LeuGlnLeuHisLeuHisTrpGlyAlaAalGlyArgProGlySerGluHisThrValGlu 242
Db 679 CTGCACTGTATCTGCATCTGGGGGCTCGAGGTGTCTCGGGCTCGAGGACACTGTGGAA 738
Qy 243 GlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAlaArgVal 262
Db 739 GGCCACCGTTTCCCTCGCGAGATCCAGTGGTTTCACTCAGCACCGCTTTTGCAGAGTT 798
Qy 263 AspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGluGly 282
Db 799 GACGAGGCTTGGGGCGCCCGGAGGCTG-GCGGTGTGGCGCTTCTTGGAGAGGAG--- 854
Qy 283 ProGluGluAsnSerAlaTyrGlnGlnLeuLeuLeuSerArgLeuGluGluIleAlaGluGlu 302
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855 CCGGAGAAACAGTGCCTATGACGAG--TTGGTCTCGCTGGWAGAAATCGCTGAGGAA 911
|||||
303 GlycerGluThrGlnValProGlyLeuAspIleSerAlaLeu 316
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912 GGT---CAGAGMTCAAGTCCAGGACTGGAMTAYTGCVTYCTG 950
|||||

RESULT 11
BX423970
LOCUS
DEFINITION
  BX423970 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
  CS0DA003YB12 5-PRIME, mRNA sequence.
ACCESSION
  BX423970
VERSION
  BX423970.2 GI:46955310
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1 (bases 1 to 916)
  Li,W.B., Gruber,C., Jesses,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
  On May 15, 2003 this sequence version replaced gi:30766328.
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
  Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
  was not normalized. Library was constructed by Life Technologies, a
  division of Invitrogen.
  This sequence belongs to sequence cluster 5300.f
  For more information about this cluster, see
  http://www.genoscope.cns.fr/cdna?s=CS1DA001ZF09QP1&c=5300.f.
FEATURES
  Location/Qualifiers
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      /clone="CS0DA003YB12"
      /tissue_type="NEUROBLASTOMA"
      /clone_lib="Homo sapiens NEUROBLASTOMA"
      /note="vector: pCMVSPORT_6; 1st strand cDNA was primed
      with a NotI-oligo(dT) primer. Five prime end enriched,
      double-strand cDNA was digested with Not I and cloned into
      the Not I and EcoRV sites of the pCMVSPORT 6 vector.
      Library was not normalized."
ORIGIN
Alignment Scores:
Pred. No.:      8.75e-109      Length:      916
Score:          1472.00      Matches:      276
Percent Similarity: 92.4%      Conservative: 5
Best Local Similarity: 90.8%      Mismatches: 23
Query Match:      60.7%      Indels:      0
DB:              5          Gaps:          0
US-09-967-237B-2 (1-459) x BX423970 (1-916)

Qy 1 MetlaProLeuCysProSerProTrieuProLeuLeuLeuProAlaProAlaProGly 20
Db 5 ATGGCTCCCTGTGCCAGCCCTGGCTCCTCTGTGTGAWCCCGCCCTGTCTCCAGGC 64
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 65 CTCACTGTGCACACGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 124
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspProLeu 60
Db 125 CCCCAGATGAGGAGGATTCCTCCCTTGGGAGGAGGCTCTWCTGGGAAGATGACCCACTG 184

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Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 185 GCGAGGAGGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGAGATTCACCCGGAGAG 244
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValValPro 100
Db 245 GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCWACCTGAAGTAAAGCCT 304
Qy 101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 305 AAATCAAGAGAGAGAGGCTCCCTGAAGTGAAGAGATCTACTACTGTGAGAGGCTCTCGGA 364
Qy 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
Db 365 GAACCTCAGAACCCAGATTAAGCCACAGGACCAAGAGAGGAGATGACAGAGTCAT 424
Qy 141 TrpArgTyroGlyGlyAspProProTrieuProArgValSerProAlaCysAlaGlyArgPhe 160
Db 425 TGGCGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 484
Qy 161 GluSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 485 CAGTCCCGGCTGGATATCCCGCCCGGCTCTGCGCGGCTCTGCGCGGCTCTGCGCGGCTCTG 544
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlnHis 200
Db 545 GAACCTCTGGGCTTCAGCTCCCGCGCTCCAGAGATGCGCTGCGCMACNATGGCCAC 604
Qy 201 SerValGlnLeuThrLeuProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 605 AGTGTGCAACTGAGCCCTCTCTGGCTAGAGAGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTG 664
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTrieuGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 665 CCGGCTCTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCA 724
Qy 241 ValGluGlyHisArgPheProAlaGluLeuHisValHisLeuSerThrAlaPheAla 260
Db 725 GTGGAAGCCACCGTTTCTCTCGGAGATCCAGTGTGTTTAMCTCARCAGCGCTTTGCC 784
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 785 ARAATTGAGGAGGCTTTGGGCGCGCGGAGGCTGCGCGCTGTGGCGCGCTTTCTGGAG 844
Qy 281 GluGlyProGluGlnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluAla 300
Db 845 GAGGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 904
Qy 301 GluGluGlySer 304
Db 905 GAGGAGGCTCA 916

RESULT 12
COS79387
COS79387 971 bp mRNA linear EST 20-JUL-2004
ILLUMIGEN MCQ 50239 Katze_WML Macaca mulatta cDNA clone
IBUW:17608 5' similar to Bases 6 to 971 highly similar to human
CA9 (Hs.63287), mRNA sequence.
COS79387
COS79387.1 GI:50410317
VERSION
  COS79387.1
KEYWORDS
  EST.
SOURCE
  Macaca mulatta (rhesus monkey)
ORGANISM
  Macaca mulatta
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Cercopithecoidea; Cercopithecinae; Macaca.
  1 (bases 1 to 971)
  Magness,C.L., Fellin,P.C., Thomas,M.J., Korth,M.J., Agv,M.B.,
  Proli,S.C., Fitzgibbon,M., Scherer,C.A., Miner,D.G., Katze,M.G. and
  Iadonato,S.P.
  Analysis of the Macaca mulatta transcriptome and the sequence
  divergence between Macaca and human

```



JOURNAL  
PURNED  
COMMENT

Genome Biol. 6 (7), R60 (2005)  
15998449  
Contact: C. Magness  
Illumigen Biosciences Inc.  
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA  
Tel: 2063780400  
Fax: 2063780408  
Email: cmagness@illumigen.com  
Sequenced on 2004.07.15. 725 Q20 bases. Library Preparation: Prof.  
Michael Katze Lab at University of Washington DNA Sequencing:  
Illumigen Biosciences Inc. For further information, see  
http://www.macaque.org

PCR Primers  
FORWARD: CCTCTACTAAGGGAACAAAA  
BACKWARD: CACTATAGGGCGAATTGGGTA  
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POLYA-No.

FEATURES

source

Location/Qualifiers  
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/lab\_host="Electromax DH10B"  
/clone\_lib="Katze MWIL"  
/note="Organ: ileum; Vector: pDONR 222; Site 1: Berg I;  
Site 2: Berg I; Created from CloneMiner cDNA Library  
Construction kit (catalog #18249-029)"

ORIGIN

Alignment Scores:

Pred. No.: 3.6e-107 Length: 971  
Score: 1452.50 Matches: 286  
Percent Similarity: 88.9% Conservative: 11  
Best Local Similarity: 85.6% Mismatches: 20  
Query Match: 59.9% Indels: 17  
DB: 7 Gaps: 2

US-09-967-237B-2 (1-459) x COS79387 (1-971)

QY 55 GlyAlaAspProLeuGlyGluAspLeuProSerGluGluAspSerProArgGlu 74  
DB 3 GGGAGATGATCCACTGCTGATGAGGAGATCTGCCAGTGAAGAGATCCACCCAGAGAG 62  
QY 75 GluAspProGlyGluGluAspLeuProGlyGluAspLeuProGlyGluGluAsp 94  
DB 63 GAGGATCCA-----CCAGAGAGGAGGAT 86  
QY 95 LeuProGluValIysProIysSerGluGluGlySerLeuIysLeuGluAspLeuPro 114  
DB 87 CTACCTGAAGTTAAGCTTAATCAGAGAGAGGCTCTCCCTGAAGTTAGAGATCTACCT 146  
QY 115 ThrValGluAlaProGlyAspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlu 134  
DB 147 ACTGTTGAGGCTCTCGAGATCCTCAAGAACCCAGAGTAATGCCACAGGACAAAGAA 206  
QY 135 GlyAspAspGlnSerHisTrpArgTyrGlyAspProProTrpProArgValSerPro 154  
DB 207 GGGGTAACACAGACACTGGCGTATGGAGGGGACCCGCCCTGGCCCGAGGTGTCCCA 266  
QY 155 AlaCysAlaGlyArgPheGlnSerProValAspIleArgProGlnLeuAlaAlaPheCys 174  
DB 267 GCCTGCCGGGGCGCTTCCAGTCCCGGTAGATATCCGCCCCAGCTCCGCCGCTTCTGC 326  
QY 175 ProAlaLeuArgProLeuGluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArg 194  
DB 327 CCCGCCCTGCGACCCCTGGAACTCTCTGGGCTTCGAGCTCCCGCTGCTCCACAGAACTGCGC 386

QY 195 LeuArgAsnAsnGlyHisSerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeu 214  
DB 387 CTGCGCAACAATGGCCACAGTGTGCAACTGACCTGCTCCGGGCTAGAGATGGCTCTG 446  
QY 215 GlyProGlyArgGluTyrArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArg 234  
DB 447 GGTCCCGGGCGGGAGTACCGGGCTCTGCAGCTGCACTCGGGGTCTGTAGGTCTGT 506  
QY 235 ProGlySerGluHisThrValGluGlyHisArgPheProAlaGluIleHisValValHis 254  
DB 507 CCGGGCTCGAGACACACTGTGGAAGGCCACCGTTTCCCTGCCGAGATCCACCGTGTAC 566  
QY 255 LeuSerThrAlaPheAlaArgValAspGluAlaLeuGlyArg-ProGlyGlyLeuAlaVa 274  
DB 567 ATCAGACCCGCTATGCCAGAGTTGGAGGGCTTTGGGGCGCCCCGGAGGCTTGGCCGT 626  
QY 274 lLeuAlaAlaPheLeuGluGluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSe 294  
DB 627 GTTGGCGGCTTTCTGGAGGAGGCCCGGAGAAACAGTGCCTATGAGCAGTTGTCTGTC 686  
QY 294 rArgLeuGluGluIleAlaGluGlySerGluThrGlnValProGlyLeuAspIleSe 314  
DB 687 TCACCTTGGAGAAATCGCTGAGAGAGGCTCAGAGACTCAGTCCCAAGGACTGGACATC 746  
QY 314 rAlaLeuLeuProSerAspPheSerArgTyrPheGlnTyrGluGlySerLeuThrPr 334  
DB 747 TGCACCTCTGCGCTCTGACCTCAGCCGCTACTTCCGATATGAGGGGTCTCTGACTACAG 806  
QY 334 oProCysAlaGlnGlyValIleTrp-ThrValPheAsnGlnThrValMetLeuSerAlaL 354  
DB 807 GCCTGTGTCAGGGGTGTCATCTGGGACTGTGTTTTACCAGACAGTGTGCTGAGTGCTA 866  
QY 354 yGlnLeuHisThrLeuSerAspThrLeu-TrpGlyProGlyAspSer-ArgLeuGlnLe 373  
DB 867 ACCACCTCCACCCCTCTCTGAAGCCCTGGGGGGGACCTGGGAGCTCTCCGGCTACGGCT 926  
QY 373 uAsnPhe---ArgAlaThrGlnProLeuAsnGly 383  
DB 927 GAACCTTCGAGAGGGAGCCACCCTTGGAGATGGG 960  
RESULT 13  
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LOCUS  
DEFINITION  
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CDNA clone CS0DK007YK10 5-PRIME, mRNA sequence.  
AL555184  
VERSION  
AL555184.3 GI:45859924  
EST.  
KEYWORDS  
Homo sapiens (human)  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
REFERENCE  
1 (bases 1 to 927)  
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
On Feb 15, 2001 this sequence version replaced gi:31276993.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqrefgenoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by life technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5300.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CS0DK007BF05Q0P1&c=5300.f.  
LOCATION/Qualifiers  
1. .927  
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/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Alignment Scores:
Pred. No.:      4,99e-103      Length:      927
Score:          1401.00       Matches:     271
Percent Similarity: 96.1%    Conservative: 2
Best Local Similarity: 95.4% Mismatches:   8
Query Match:    57.8%      Indels:      5
DB:              1           Gaps:       1

US-09-967-237B-2 (1-459) x AL555184 (1-927)

Qy   3   ProLeuCysProSerProTrrPLeuProLeuLeuLeuProAlaProAlaProGlyLeuThr 22
Db   37  CCCCTGTGCCAGCCCGCTGGCTCCTCTGTGTATCCCGCCCCCTGCCTCCAGGCTCACT 96

Qy   23  ValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeuProArg 42
Db   97  GTCCAACTGCTGTGTACATGCTGTTCTTGTTGGTCCTGTCCATCCCGAGGTTGCCCGG 156

Qy   43  MetGlnGluAspSerProLeuGlyGlySerSerglyGluAspAspProLeuGlyGlu 62
Db   157  ATGCAGGAGATTCCCTTGGAGGAGGCTCTCTCTGGGAAGATGACCACACTGGCGAG 216

Qy   63  GluAspLeuProSerGlnGluAspSerProArgGluGluAspProProGlyGluGluasp 82
Db   217  GAGGATCTGCCCATGAAGAGATTACCCAGAGAGAGATCCACCCGGAGAGAGGAT 276

Qy   83  LeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValValProLysSer 102
Db   277  CTACCTGGAGAGAGGATCTACTGGAGAGAGGATCTACCTGAAGTTAAGCTTAATCA 336

Qy   103  GluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGlyAspPro 122
Db   337  GAAGAAGAGGCTCCCTGAAGTTAGAGGATCTACCTACTGTTGAGGCTCTCTGGAGATCCT 396

Qy   123  GlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHisTrpArg 142
Db   397  CAAGAACCCAGAAATAATGCCACAGGGACAAGAAGGGAGTGACACAGAGTCATTGGCGC 456

Qy   143  TyrGlyGlyAspProProTrrPProArgValSerProAlaCysAlaGlyArgPheGlnSer 162
Db   457  TATGGAGGGGACCCCGCTTGGCCCGGGGTGCCAGCCCTGGCGGGCGCTTTCAGTCC 516

Qy   163  ProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeuGluLeu 182
Db   517  CCGGTGGATATCGCCCCCAGCTCGCGCTTCTGCGCGGCTTGGCGGCTTGGAACTC 576

Qy   183  LeuGlyPheGlnLeuProProLeuProGluLeuLeuArgLeuArgAsnAsnGlyHisSerVal 202
Db   577  CTGGGCTTCAGCTCCCGCGCTCCAGAACTCGCGCTTCGCAACAATGGCCACAGTGTG 636

Qy   203  GlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTrpArgAla 222
Db   637  CAATGACCTGCTCTTGGGCTTAGAGATGGCTCTTGGGTTCCTGGGGGGAGTACCGGGCT 696

Qy   223  LeuGlnLeuHisLeuHisTrp-GlyAlaAlaGlyArgProGlySerGluHisThrValGln 242
Db   697  CTCAGCTGCATCTGCACCTGGGGGGCTCGAGTCTGTCGGGCTCGGAGCACACTGTGGA 756

Qy   242  uGlyHisArgPheProAlaGluLeuHisValValHisLeuSerThrAlaPheAlaArgVa 262
Db   757  AGGCCACCGTTTTCCCTGCCGAGATCCACGTGGTGTACYC-AGCACASCTTTTGGCAGAGT 815

```

Qy	61	GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu	80																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																			
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Db 662 CTGAGTCTAAGCAGCTCCACACCCTCTCTGACTCCCTGTGGGACCTGATGACTCTCGG 721  
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Db 722 CTGCAGCTGAACCTCCGAGCTACGAGCCTTTGAATGGGCGAATAATTGAGGCCTCCTTC 781  
Qy 391 ProAlaGlyValAspSerSerProArgAlaAlaGluProValGlnLeuAsnSerCysLeu 410  
Db 782 CCCGCTGGCGTGGATGGCAGCCCTAGGACTGTGTGACCAAGTCCACCTGAATTCTGTCTC 841  
Qy 411 AlaAlaGlyAspIleLeuAlaLeuValPheGlyLeuLeuPheAla 425  
Db 842 GCTGCTGGCGACATCCTGNCCTGGTTTTTGGGCTCCTCTTTGCT 886

Search completed: February 17, 2006, 18:21:44  
Job time : 5591 secs

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 17, 2006, 15:10:31 ; Search time 316 Seconds  
(without alignments)

2581.965 Million cell updates/sec

Title: US-09-967-237B-2

Perfect score: 2424

Sequence: 1 MAPLCPSPWLLIPAPAPG.....RRGTGGVSRPAEVAETGA 459

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -OPT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
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-HOST=abs06p -USER=US09967237 @CCN 1 1 290 @runat\_15022006\_182246\_28055  
-NCPU=6 -ICPU=3 -NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*

1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/PCTUS COMB.seq.\*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2424	100.0	1522	2	US-08-481-658B-1
2	2424	100.0	1522	2	US-08-477-504A-1
3	2424	100.0	1522	2	US-08-486-756A-1
4	2424	100.0	1522	2	US-08-485-862B-1
5	2424	100.0	1522	3	US-08-787-739-1
6	2424	100.0	1522	3	US-08-487-077A-1
7	2424	100.0	1522	3	US-08-485-863A-1
8	2424	100.0	1522	3	US-08-485-049D-1
9	2424	100.0	1522	3	US-09-178-115-1

10	2424	100.0	1522	3	US-09-177-776-1	Sequence 1, Appli
11	2424	100.0	1522	3	US-09-772-719B-1	Sequence 1, Appli
12	2424	100.0	1522	3	US-08-260-190-5	Sequence 5, Appli
13	2424	100.0	1522	3	US-09-949-016-171	Sequence 171, App
14	2420	99.8	1552	3	US-09-949-016-4332	Sequence 4332, Ap
15	2233	92.1	5052	3	US-08-260-190-23	Sequence 23, Appli
16	2227	91.9	1399	3	US-08-335-469-1	Sequence 1, Appli
17	2227	91.9	1399	3	US-08-260-190-1	Sequence 1, Appli
18	2036	84.0	1397	6	US-07-964-589-1	Sequence 1, Appli
19	2036	84.0	1397	6	PCT-US93-02024-1	Sequence 11913, A
20	1253.5	51.7	11237	3	US-09-949-016-11913	Sequence 16074, A
21	1253.5	51.7	11237	3	US-09-949-016-16074	Sequence 5, Appli
22	1176.5	48.5	10898	2	US-08-481-658B-5	Sequence 5, Appli
23	1176.5	48.5	10898	2	US-08-477-504A-5	Sequence 5, Appli
24	1176.5	48.5	10898	2	US-08-486-756A-5	Sequence 5, Appli
25	1176.5	48.5	10898	2	US-08-485-862B-5	Sequence 5, Appli
26	1176.5	48.5	10898	3	US-08-787-739-5	Sequence 5, Appli
27	1176.5	48.5	10898	3	US-08-487-077A-5	Sequence 5, Appli
28	1176.5	48.5	10898	3	US-08-485-863A-5	Sequence 5, Appli
29	1176.5	48.5	10898	3	US-08-485-049D-5	Sequence 5, Appli
30	1176.5	48.5	10898	3	US-09-178-115-5	Sequence 5, Appli
31	1176.5	48.5	10898	3	US-09-177-776-5	Sequence 5, Appli
32	1176.5	48.5	10898	3	US-09-772-719B-5	Sequence 5, Appli
33	714	29.5	415	2	US-08-481-658B-28	Sequence 28, Appli
34	714	29.5	415	2	US-08-477-504A-28	Sequence 28, Appli
35	714	29.5	415	2	US-08-486-756A-28	Sequence 28, Appli
36	714	29.5	415	2	US-08-485-862B-28	Sequence 28, Appli
37	714	29.5	415	3	US-08-487-077A-28	Sequence 28, Appli
38	714	29.5	415	3	US-08-485-863A-28	Sequence 28, Appli
39	714	29.5	415	3	US-08-485-049D-28	Sequence 28, Appli
40	714	29.5	445	3	US-08-787-739-28	Sequence 28, Appli
41	714	29.5	445	3	US-09-178-115-28	Sequence 28, Appli
42	714	29.5	445	3	US-09-177-776-28	Sequence 28, Appli
43	714	29.5	445	3	US-09-772-719B-28	Sequence 28, Appli
44	629	25.9	1401	2	US-08-481-658B-49	Sequence 49, Appli
45	629	25.9	1401	2	US-08-477-504A-49	Sequence 49, Appli

#### ALIGNMENTS

#### RESULT 1

US-08-481-658B-1

; Sequence 1, Application US/08481658B

; Patent No. 5955075

; GENERAL INFORMATION:

; APPLICANT: Zavada, Jan

; APPLICANT: Pastorekova, Silvia

; APPLICANT: Pastorek, Jaromir

; TITLE OF INVENTION: MN Gene and Protein

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leona L. Lauder

; STREET: 6 Mariposa Court

; CITY: Tiburon

; STATE: California

; COUNTRY: USA

; ZIP: 94920

; COMPUTER READABLE FORM: disk

; MEDIUM TYPE: Floppy

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/481,658B

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/260,190

; FILING DATE: 15-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863

; REFERENCE/DOCKET NUMBER: D-0021.3E



```
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-477-504A-1

Alignment Scores:
Pred. No.: 7.5e-197 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 2
DB:

US-09-967-237B-2 (1-459) x US-08-477-504A-1 (1-1522)

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DB 13 ATGGCTCCCTGTGCCAGCCCTGGCTCCCTCTGTGATCCGCGCCCTGTCCAGGC 72
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QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
DB 193 GCGGAGGAGGATTCGCCAGTGAAGAGATTCACCCAGAGAGGAGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
DB 253 GAGGATCTACTGGAGAGGAGATCTACCTGGAGAGGAGATCTACTGGAATTAAGCCT 312
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QY 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
DB 373 GATCCTCAAGAACCCCAAGATATGCCCAAGGACAAAGAGGGGATGACCAAGATCAT 432
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QY 221 ArgAlaLeuGlnLeuHisLeuHisLeuHisLeuHisLeuHisLeuHisLeuHisLeuHis 240

; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; US-08-477-504A-1

Alignment Scores:
Pred. No.: 7.5e-197 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
Gaps: 2
DB:

US-09-967-237B-2 (1-459) x US-08-477-504A-1 (1-1522)

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DB 73 CTCACTGTGCACTGTGCTGTCTCACTGCTCTTCTGATGCTCTGATCCCAAGAGGTTG 132
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DB 133 CCCCGAGTGCAGAGGATTCCTCTGGAGAGGCTCTTCTGGGAGAGATGATCCCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
DB 193 GCGGAGGAGGATTCGCCAGTGAAGAGATTCACCCAGAGAGGAGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
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DB 313 AATCAGAGAGAGGCTCCCTGAGTTAGAGATCTACTACTGTGAGGCTCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
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DB 493 CAGTCCCGGTGGATATCCGCCCCCAGCTGCCGCTCTTCTGCCGCGCTTGGCGCCCTG 552
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QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyArgGluTyr 220
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QY 221 ArgAlaLeuGlnLeuHisLeuHisLeuHisLeuHisLeuHisLeuHisLeuHisLeuHis 240

673 CGGGCTCTGCAGCTGCATCTGCACCTGGGGGGCTGCAGGTCGTCCGGGCTCGGAGCACACT 732
241 ValGluGlyHisArgPheProAlaGluLeuHisValValHisLeuSerThrAlaPheAla 260
733 GTGGAAGGCACCGTTTCCCTCCGAGATCCAGTGTTTCCCTCAGCACCGCTTTGGCC 792
261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
793 AGAGTTGACGAGGCTTTGGGCGCGCGGAGGCTGGCCGTGTGGCCGCTTTCTGGAG 852
281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluLeuAla 300
853 GAGGGCCCGAAGAAACAGTGCCTATGAGCAGTGTGCTGCTGCTGCTGGAAGAAATCGCT 912
301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
913 GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGAGCATATCTGCACCTCTCTGCTCTGAC 972
321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrProProCysAlaGlnGlyVal 340
973 TTCAGCGGCTACTTCCAATATGAGGGGTCTCTGACTACACCGGCTGTGCCAGGGTGTG 1032
341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
1033 ATCTGACCTGTGTTAAACCAAGACAGTGTGCTGAGTGTGCTGAGTGTGCTGAGTGTGCT 1092
361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
1093 GACACCTGTGGGACCTGTGACTCTCGGCTACAGTGAACCTTCGAGGCGAGCGACGCT 1152
381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
1153 TTGAATGGGCGAGTGATTGAGGCTCTTCCCTGCTGGAGTGGACAGCAGTCTCTGGGCT 1212
401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
1213 GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
1273 GGCTCTCTTTTGTCTGTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
1333 AGGGAACCAAGGGGCTGTGAGTACCAGCCAGCAGAGGTAGCCGAGACTGGAGCC 1389

RESULT 3
US-08-486-756A-1
; Sequence 1, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-486-756A-1

Alignment Scores:
Pred. No.: 7.5e-197 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 2 Gaps: 0

US-09-967-237B-2 (1-459) x US-08-486-756A-1 (1-1522)

QY 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuLeuProAlaProGly 20
DB 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCTCTGTGATCCCGGCCCTGTCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 73 CTCACTGTGCNACTGCTGCTGCTCACTGCTCTCTGATGCTCTGCATCCCGAGAGTTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspProLeu 60
DB 133 CCCGGATGCAGGAGGATCCCCCTTGGGAGGAGGCTCTTCTGGGAAGATGACCCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
DB 193 GCGGAGGAGGATGCCCCAGTGAAGAGGATTCACCCAGAGAGGATCCACCCGGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
DB 253 GAGGATCTACTGGAGGAGGAGGATCTACCTGGAGAGGAGGATCTACTGAGTTAAGCCT 312
QY 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
DB 313 AAATCAGAAGAGGAGGCTCCCTGAGTTAGAGGATCTACTACTGTTGAGGCTCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
DB 373 GATCCTCAAGAACCCCAAGATAATGCCCAAGGACAAAGAGGATGACCAAGAGTCAT 432
QY 141 TrpArgTrcGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
DB 433 TGGCGCTATGGAGGAGGACCCCGCTCTGGCCCCGGGTGTCCACGCTTGGCGGGCCGCTTC 492
QY 161 GlnSerProValAspLeuArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB 493 CAGTCCCCGGTGGATATCCGCCCCAGCTCGCCGCTTCTGCGCGGCTGCGCCCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProLeuArgLeuArgAsnGlnHis 200
DB 553 GAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGGCGCAACATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
DB 613 AGTGTGCNACTGACCTTGCCTCTCTGGGCTAGAGATGGCTCTGGGTCCCGGGCGGAGTAC 672
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QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240
DB 673 CGGGCTCTGCAGCTGCATCTGCACCTGGGGGGTGCAGGTCTGTCGGGCTCGGAGCACACT 732
QY 241 ValGluGlyHisArgPheProAlaGluLileHisValValHisLeuSerThrAlaPheAla 260
DB 733 GTGGAAGGCCACCGTTTCCCTCCGAGATCCAGTGTGTTACCTCAGCACCGCTTGTGCC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
DB 793 AGAGTTGACGAGGCCCTTGGGGCGCCCGGAGGCTGTCGCCGTGTGGCCGCTTCTGGAG 852
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluLileAla 300
DB 853 GAGGGCCCGGAAGAAACACAGTGCCTATGAGCAGTGTCTGCTGCTTGAAGAAATCGCT 912
QY 301 GluGluGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
DB 913 GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCATCTCTGCCCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrProProCysAlaGlnGlyVal 340
DB 973 TTCAGCCGCTACTTCCCAATATGAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGT 1032
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
DB 1033 ATCTGACTGTGTAAACACAGACAGTGTGCTGAGTGTCTAAGCAGCTCCACACCTCTCT 1092
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
DB 1093 GACACCTGTGGGACCTCTGTGACTCTCGCTACAGCTGAACCTTCGAGCGACGAGCCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
DB 1153 TTGAATGGCGAGTGATTCAGGCTCTTCCCTGCTGGAGTGGACAGAGTCTCTCGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
DB 1213 GCTGAGCAGTCCAGCTGAATTCCTGCTGGCTGTGTGACATCTCTAGCCCTGTGTTTT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
DB 1273 GGCTCTCTTTTGTCTGTACACGCTGCGCTTCTTGTCCAGATGAGAAGGACGACAGA 1332
QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
DB 1333 AGGGGAACCAAGGGGTGTGAGCTACCCGCCAGCAGAGGTAGCCGAGACTGGAGCC 1389
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## RESULT 4

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US-08-485-862B-1
; Sequence 1, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,862B
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Db 1273 GGCTCTCTTTGCTGTCACAGCGTCCGCTTCCTTGTGCAGATGAGAGCGACACAGA 1332  
Qy 441 ArgGlyThrIysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459  
Db 1333 AGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACTGGAGCC 1389

RESULT 8  
US-08-485-049D-1  
; Sequence 1, Application US/08485049D  
; Patent No. 6204370  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/485,049D  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1522 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-485-049D-1

Alignment Scores:  
Pred. No.: 7 5e-157 Length: 1522  
Score: 2424.00 Matches: 459  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0

US-09-967-237B-2 (1-459) x US-08-485-049D-1 (1-1522)

Qy 1 MetAlaProLeuCysProSerProTrrProLeuProLeuLeuLeuProAlaProGly 20  
Db 13 ATGGCTCCCTGTGCGCCAGCCCTGGCTCCCTCTGTGTGATCCCGGCCCTGTCTCCAGGC 72  
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40  
Db 73 CTCAGTGTCACTGTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132  
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspProLeu 60

133 CCCCAGATCAGAGGATTCCTTGGGAGGAGGCTCTTCTGGGAGAGATGACCCACTG 192  
61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80  
193 GCGAGAGAGATCTGCCAGTGAAGAGGATTCACCCAGAGAGAGGATTCACCCGAGAG 252  
81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100  
253 GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCT 312  
101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120  
313 AAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGGATCTACTACTGTTGAGGCTCTCGGA 372  
121 AspProGlnGluProGlnAenAenAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
373 GATCCTCAAGAACCCAGAGATTAATGCCACAGGACAAAGAGGAGATGACACAGATCAT 432  
141 TrpArgTyrGlyGlyAspProProTrrProArgValSerProAlaCysAlaGlyArgPhe 160  
433 TGGCGCTATGAGAGCGACCCCGCTGCGCCCGGGTGTCCACAGCCTGCGCGCGCTTC 492  
161 GlnSerProValAspLysArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180  
493 CAGTCCCGGTGATATCGCCCGCCAGCTCGCCCGCTTCTGCGCGGCTCGCGCCCGCTG 552  
181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgLeuAenGlyHis 200  
553 GAACTCTGGGCTTCAGCTCCCGCGCTCCCAAGACTCGCGCTCGCGCAACATGGCCAC 612  
201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220  
613 AGTGTCAACTGACCTGCTCTGGGCTAGAGATGCTCTGGGTCGCGGCGGAGTAC 672  
221 ArgAlaLeuGlnLeuHisHisTrrGlyAlaAlaGlyArgProGlySerGluHisThr 240  
673 CGGGCTCTGCAGCTGCATCTGCACATGGGGGCTGCAGGCTGCTCGGCTCGGACACACT 732  
241 ValGluGlyHisArgPheProAlaGluLeuHisValValHisLeuSerThrAlaPheAla 260  
733 GTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTTGTTTCCCTCAGCACCGCTTTTGGC 792  
261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280  
793 AGAGTTGACGAGGCTTGGGGCGCCGCGGAGGCTTGGCGGTGTTGGCGGCTTCTGAG 852  
281 GluGlyProGluGluAenSerAlaTyrGluGlnLeuLeuSerArgLeuGluLysAla 300  
853 GAGGGCCCGGAGAGAACAGTGCCTATGAGCAGTTGCTGTCTGCTTGGAGAAATCGCT 912  
301 GluGluGlySerGluThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320  
913 GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCATCTCTGCCCTCTGAC 972  
321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340  
973 TTCAGCGGCTACTTCCATATAGGGGCTCTCTGACTACACCGCCCTGTGCCAGGGTGT 1032  
341 IleTrrThrValPheAenGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
1033 ATCTGAGCTGTGTTAAACAGACAGTGCCTGAGTGCCTGAGTGCCTGAGTGCCTGAGTGCCT 1092  
361 AspThrLeuTrrProGlyProGlyAspSerArgLeuGlnLeuAenPheArgAlaThrGlnPro 380  
1093 GACACCTGTGGGAGACTGTGTGACTCTGCGCTACAGCTGAACCTCCGAGGAGCGACGCT 1152  
381 LeuAenGlyArgValLysLeuGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
1153 TTGAATGGGCGAGTGTATGAGGCTCTCTTCCCTGCTGGAGTGGACAGCAGCTCTCGGGCT 1212  
401 AlaGluProValGlnLeuAenSerCysLeuAlaAlaGlyAspLysLeuAlaLeuValPhe 420





1093	Db	GACACCTCTGGGGACCTCGTGTGACTCTCGGCTACAGCTGAACTCTCCAGCGAGCGAGCCT	1152
381	QY	LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla	400
1153	Db	TTGAATGGGCGAGTGATTGAGGCTCTCTTCCTGCTGGAGTGGACAGCATCTCTGGGCT	1212
401	QY	AlaGluProValGlnLeuAsnSerCysLeuAlaGlyAspIleLeuAlaLeuValPhe	420
1213	Db	GCTGAGCCAGTCAGCTGAATTCCTCGCTGGCTGCTGGTGACATCTTAGCCCTGGGTTTT	1272
421	QY	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440
1273	Db	GGCTCTCTTTTGTCTCACACAGCTCGCTTCTCTGTGCAGATGAGAGCGACGACAGA	1332
441	QY	ArgGlyThrIysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla	459
1333	Db	AGGGCAACCAAGGGGGTGTGAGTCTACGCCACAGCAGAGTAGCCAGACTGGAGCC	1389

RESULT 10

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US-09-177-776-1
US-09-177-776-1
Sequence 1, Application US/09177776A
Patent No. 6297051
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
FILE REFERENCE: D-0021.5A
CURRENT APPLICATION NUMBER: US/09/177,776A
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 08/787,739
EARLIER FILING DATE: 1997-01-24
EARLIER APPLICATION NUMBER: 08/485,049
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/486,756
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/477,504
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/481,558
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/485,862
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/485,863
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/487,077
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/260,190
EARLIER FILING DATE: 1994-06-15
EARLIER APPLICATION NUMBER: 08/177,093
EARLIER FILING DATE: 1993-12-30
EARLIER APPLICATION NUMBER: 07/964,589
EARLIER FILING DATE: 1992-10-21
EARLIER APPLICATION NUMBER: PW-709-92
EARLIER FILING DATE: 1992-03-11
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1522
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (13)..(1389)
FEATURE:
NAME/KEY: mat.peptide
LOCATION: (124)..(1389)
US-09-177-776-1

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Alignment Scores:	
Pred. No.:	7.5e-197
Score:	2424.00
Best Similarity:	100.0%
Best Local Similarity:	100.0%
Length:	1522
Matches:	459
Conservative:	0
Mismatches:	0

Query Match:	100.0%	Indels:	0
DB:	3	Gaps:	0
US-09-967-237B-2 (1-459) x US-09-177-776-1 (1-1522)			
Qy	1	MetAlaProLeuLeuCysProSerProTTPLeuProLeuLeuIleProAlaProAlaProGly	20
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Qy	21	LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu	40
Db	73	CTCACTGTGCAACTGCTGTCTCACTGTCTCTGTATGCTCTCATCCCCAGAGGTTG	132
Qy	41	ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu	60
Db	133	CCCCGATGCAGGAGATTCCTCCCTTGGAGAGGCTCTCTGGGGAAGATGACCCACTG	192
Qy	61	GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu	80
Db	193	GGCGAGAGATCTGCCAGTGNAGAGATTACCCAGAGAGGAGATCCACCCGAGAG	252
Qy	81	GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluVallysPro	100
Db	253	GAGGATCTACTGGAGAGGAGATCTACCTGGAGAGGAGATCTACCTGAAGTTAAGCCT	312
Qy	101	LysSerGluGluGlySerLysLeuGluAspLeuProThrValGluAlaProGly	120
Db	313	AAATCAGAAAGAGGGCTCCCTGAAGTTAGAGATCTACCTACTGTGAGGCTCTCGGA	372
Qy	121	AspProGlnGluProGlnAenAenAlaHisArgAspLysGluGlyAspAspGlnSerHis	140
Db	373	GATCTCTCAGAACCCAGAAATAATGCCCCACAGGACAAAGAGGGGATGACCCAGATCAT	432
Qy	141	TrpArgTyrGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe	160
Db	433	TGGCGCTATGGAGGCGACCGCCCTGGCCCGGGTGTCCACGCTGCGGGCCGCTTC	492
Qy	161	GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu	180
Db	493	CAGTCCCGGTGATATCCGCCCCAGCTGCGCCCTTCTGCCCGGCCCTTGCGCCCTCG	552
Qy	181	GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAenGlyHis	200
Db	553	GAATCTCTGGGCTTCAGACTCCCGCGCTCCAGAACTGGGCTGCGCAACATGGCCAC	612
Qy	201	SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr	220
Db	613	AGTGTGCAACTGACCTCGCTCTCTGGGCTAGAGATGGCTCTGGGTCTCCGGCGGGAGTAC	672
Qy	221	ArgAlaLeuGlnLeuHisLeuHisTTPGlyAlaAlaGlyArgProGlySerGluHisThr	240
Db	673	CGGGCTCTGCAGTGCATCTGCAGCTGGGGGGCTGCGAGGTCGTCCGGCTCGGAGCACCT	732
Qy	241	ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla	260
Db	733	GTGGAAGCCACCGTTTCTTCCGCGAGATCCAGTGGTTCACTCAGCACCGCTTTGCC	792
Qy	261	ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu	280
Db	793	AGAGTTGACGAGGCTTGGGGCGCCGGGAGGCTGGCCGTGTGGCGGCTTTCTGGAG	852
Qy	281	GluGlyProGluAenSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla	300
Db	853	GAGGGCCCGAAGAAACAGTGGCTATGACAGTGTCTGTCTCGTTGGGAAGAAATCGCT	912
Qy	301	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp	320
Db	913	GAGGAAGGCTCAGACTCAGGTCACAGGATCGACATATCTCACTCTCTGCTCTCTGAC	972
Qy	321	PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal	340
Db	973	TTTACGGCTACTTCCAAATGAGGGGTCTTGACTACACGGCCCTGTGCCAGGGGTGC	1032

QY 341 IletpThrValPheAanGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
Db 1033 ATCTGGAGTGTGTTTAAACAGACAGTGTCTGAGTCTAAGCAGCTCCACACCCCTCTCT 1092  
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAenPheArgAlaThrGlnPro 380  
Db 1093 GACACCCCTGTGGGAGCTGTGTGACTCTCGGTACAGCTGAACCTCCGAGCGACGACCT 1152  
QY 381 LeuAenGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
Db 1153 TTGAATGGGAGTGTGTTGAGGCTCTCTCCCTGCTGAGTGGACAGCAGCTCTCGGGCT 1212  
QY 401 AlaGluProValGlnLeuAenSerCysLeuAlaGlyAspIleLeuAlaLeuValPhe 420  
Db 1213 GCTGAGCCAGTCCAGCTGAATCTCTGCTGGCTGTGCTGACATCTTAGCCCTGGTGT 1272  
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440  
Db 1273 GGCTCTCTTTTGTGTCCACGCGTGCCTTCTTGTGAGATGAGAGCGACACAGA 1332  
QY 441 ArgGlyThrLysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459  
Db 1333 AGGGAAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACTGGAGCC 1389

## RESULT 11

US-09-772-719B-1  
; Sequence 1, Application US/09772719B  
; Patent No. 6770438  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; Pastorekova, Silvia  
; Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 465 California Street, Suite 450  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719B  
; FILING DATE: 30-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3A-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1522 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-772-719B-1  
Alignment Scores:

Pred. No.: 7 Se-197 Length: 1522  
Score: 2424.00 Matches: 459  
Percent Similarity: 100.0% Conservatives: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 3 Gaps: 0  
US-09-967-237B-2 (1-459) x US-09-772-719B-1 (1-1522)  
QY 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuLeuProLaProAlaProGly 20  
Db 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGATCCCGCCCTGTCTCCAGGC 72  
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40  
Db 73 CTCACCTGTGCAACTGTCTGTCTACTGCTGCTTCTGTATGCTCTCATCCCCAGAGGTTG 132  
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu 60  
Db 133 CCCCCGATGAGAGGAGATTCCCCCTTGGAGAGAGGCTCTTCTGGGGAAGATGACCCACTG 132  
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80  
Db 193 GCGAGAGGAGATCTGCCAGTGAAGAGGATTCAACCAGAGAGGAGATCCACCCGAGAG 252  
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100  
Db 253 GAGGATCTACCTGGAGAGGAGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCT 312  
QY 101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120  
Db 313 AAATCAGAAAGAGAGGGCTCCCTGAAGTTAGAGGATCTACCTACTGTGTAGGGCTCTTGA 372  
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
Db 373 GATCTCTCAAGAACCCAGAAATTAATGCCACAGGGAACAAGAGGGGATGACACAGTTCAT 432  
QY 141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160  
Db 433 TGGCGCTATGAGAGGCGACCCGCTGGCGCCCGGGTGTCCACAGCTTCGCGGGCGCTTC 492  
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180  
Db 493 CAGTCCCCGGTGGATATCCGCCCCAGCTCGCGCCCTTCTGCCCGGCCCTTGGCCCCCTG 552  
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlnHis 200  
Db 553 GAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTGCGCAACAATGGCCAC 612  
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220  
Db 613 AGTGTGCAACTGACCTTGCTCTCTGGGCTTAGAGATGGCTCTGGGCTCCCGGGGGAGTAC 672  
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240  
Db 673 CGGGCTCTGCAGCTGCATCTGCACCTGGGGGGCTGCAGGTCGTCGGGGCTCGGAGCACACT 732  
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260  
Db 733 GTGGAAGGCCACCGCTTTCCTCCGAGATCCACGTGTTTCACTCAGCACCGCTTTTGCC 792  
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280  
Db 793 AGAGTTGACGAGGCTTGGGGCGCCCGGAGGCGCTGGCGCTGTGTTCGCCCTTTCTGGAG 852  
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluLeuAla 300  
Db 853 GAGGGCCCGAAGAAACAGTGCCTATGAGCAGTTGCTCTCTCGCTTGAAGAAATCGCT 912  
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320  
Db 913 GAGGAAGGCTCAGAGACTCAGGTCCCGAGACTGGACATATCTGCATCTCTCGCTCTGAC 972

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QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340
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QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
Db 1033 ATCTGACGTGTGTTAAACACAGACAGTGTCTGAGTGTCTAAGCAGCTCCACACCCCTCTCT 1092
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCCCTGTGGGAGCTGTGTGACTCTCGGTACTACGTGAACCTTCGAGCGACGAGCCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGCGAGTGATGAGGCTCTCTCCCTGCTGGAGTGGACAGCAGTCTCTGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCCAGTCCAGCTGAATCTCTGCTGGCTGCTGGTGACATCTAGCCCTGGTTTTT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCCTCTTTTGTCTGTACACAGCTGCGCTTCTTGTGCAGATGAGAGGCAGCACAGA 1332
QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGGAACCAAGAGGGGTGTGAGCTACCGCCACGAGAGTAGCCGAGAGCTGGAGCC 1389
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## RESULT 12

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US-08-260-190-5
; Sequence 5, Application US/08260190A
; Patent No. 6774117
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/08/260,190A
; CURRENT FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)
US-08-260-190-5
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Alignment Scores:
Pred. No.: 7,5e-197 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
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US-09-967-237B-2 (1-459) x US-08-260-190-5 (1-1522)

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QY 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProGly 20
Db 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTGTGATCCGGGCCCTGTCTCCAGGC 72
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QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGTCAACTGCTGTGTCTGCTGCTTCTGATGCTGTCCATCCCAAGAGGTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspProLeu 60
Db 133 CCCCGGATGCAGGAGGATTTCCCTTGGGAGGAGGCTCTTCTGGGGAAGATGACCCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 193 GCGAGGAGGATCTGCCAGTAGAGGATTCACCCAGAGAGGAGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
Db 253 GAGGATCTACTGGAGAGGAGGATCTACTCTGGAGAGGAGATCTACTGAAGTTAAGCCT 312
QY 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGGATCTACTACTGTTGAGGCTCTCGGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
Db 373 GATCTCTCAGAAACCCAGAAATAATGCCACAGGACAAAGAGGGATGACACAGATCAT 432
QY 141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCGTATGAGAGGAGCCCGCCCTGGCCCGGGTGTCCCCAGCCTGCGGGGCCGCTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGGATATCCGCCGCCAGCTCGCGCCCTTCTGCCCGGCCCTTCGCGCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200
Db 553 GAACTCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGCGCTCGCAACAATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 613 AGTGTGCACTGACCTGCTCTCTGGCTAGAGATGGCTCTGGTCCCGGGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 673 CCGGCTCTGCAGCTGCATCTGCACATGGGGGCTGCAGGTGCTCGGGCTCGAGACACACT 732
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTTCCCTGCGGAGATCCACGTGGTTTCCCTCAGCACCGCTTTGCC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACGAGGCCCTTGGGGGCCCGGGAGGCTGGCCGTGTGGCCGCTTCTTGAG 852
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluIleAla 300
Db 853 GAGGGCCCGGAGAAACAGTGTCTATGACAGTGTCTGTCTGCTTGGGAAGAAATCGCT 912
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGACTCAGGTCCCGAGGACTGGACATATCTGACATCTCCCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340
Db 973 TTCAGCGCTACTTCCAAATATAGGGGTCTCTGACTACACCGCCCTGTGCCAGGGGTGTC 1032
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
Db 1033 ATCTGACGTGTGTTAAACACAGACAGTGTCTGAGTGTCTAAGCAGCTCCACACCCCTCT 1092
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCCCTGTGGGAGCTGTGTGACTCTCTGGCTACAGCTGAATCTCCGAGCAGCAGCCT 1152
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Qy	381	Leu	en	g	l	y	A	r	g	V	a	l	i	e	s	u	a	s	e	r	P	r	o	a	l	a	s	e	r	P	r	o	a	r	g	A	l	a	400				
Db	1153	T	T	G	A	T	G	G	C	A	G	T	G	A	T	T	G	C	C	T	T	C	C	T	T	G	C	T	G	A	G	T	G	A	G	C	A	G	1212				
Qy	401	A	a	G	l	u	P	r	o	V	a	l	G	l	u	e	n	S	e	r	C	y	s	L	e	u	A	a	A	G	l	y	A	s	p	i	l	e	u	A	l	a	420
Db	1213	G	C	T	G	A	G	C	A	G	T	C	A	A	T	T	C	T	G	C	T	G	G	T	G	C	T	G	C	T	G	A	C	A	T	C	T	A	G	C	C	1272	
Qy	421	G	l	y	L	e	u	L	e	u	P	h	e	A	l	a	V	a	l	T	h	r	S	e	r	V	a	l	a	P	h	e	L	e	u	V	a	l	G	l	u	440	
Db	1273	G	G	C	T	C	T	T	T	T	G	C	T	G	T	C	A	C	A	G	C	G	T	C	G	G	T	T	C	T	T	G	T	G	C	A	G	A	G	1332			
Qy	441	A	r	g	G	l	y	T	h	r	L	y	s	G	l	y	V	a	l	S	e	r	T	y	R	g	P	r	o	a	G	l	u	V	a	l	A	l	a	G	l	u	459
Db	1333	A	G	G	G	A	A	C	A	A	G	G	G	G	T	G	A	G	T	A	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	C	1389			

RESULT 13

US-09-949-016-171

; Sequence 171, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949, 016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241, 755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237, 768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231, 498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 171

; LENGTH: 1552

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-171

Alignment Scores:

Pred. No.: 7,72e-197 Length: 1552

Score: 2424.00 Matches: 459

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 100.0% Indels: 0

DB: 3 Gaps: 0

US-09-967-237B-2 (1-459) x US-09-949-016-171 (1-1552)

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Db	43	A	T	G	C	T	C	C	C	T	G	T	G	C	C	C	C	A	G	C	C	C	T	G	G	T	C	C	C	T	G	T	G	A	T	C	C	G	C	C	C	T	G	102					
Qy	21	L	e	u	T	h	r	V	a	l	G	l	u	L	e	u	L	e	u	S	e	r	L	e	u	L	e	u	L	e	u	M	e	t	P	r	o	V	a	l	H	i	P	r	o	G	l	u	40
Db	103	C	T	C	A	T	G	T	G	C	A	A	T	G	C	T	G	C	T	G	C	T	G	C	T	G	C	T	G	C	T	G	C	A	T	G	C	C	C	C	C	C	A	G	162				
Qy	41	P	r	o	A	r	g	M	e	t	G	l	u	A	s	p	S	e	r	P	r	o	L	e	u	G	l	y	S	e	r	S	e	r	G	l	y	A	s	p	P	r	o	L	e	u	60		
Db	163	C	C	C	G	A	T	G	C	A	G	A	G	A	T	T	C	C	C	C	T	T	G	G	A	G	A	G	C	T	T	T	G	G	A	G	A	G	C	A	T	G	222						
Qy	61	G	l	y	G																																												

343	Db	AAATCAGAGAGAGGGCTCCCTGAGATTAGAGATCTACTACTGTTGAGGCTCTGGG	402
121	Qy	AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis	140
403	Db	GATCCTCAAGAAACCCAGAAATAATGCCCCACAGGACAAAGAGGGGATGACCAAGATCAT	462
141	Qy	TtpArgTyrGlyGlyAspProProTtpProAtqValSerProAlaCysAlaGlyArgPhe	160
463	Db	TGGCGCTATGAGAGCGACACCGCCCTGGCCCGGGGTGTCCCAGCCTGCGCGGCCCGCTTC	532
161	Qy	GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu	180
523	Db	CAGTCCCGGTGGATATCGCGCCCCAGCTCGCCGCTTCTGCCCGCGCCCTGCGCCCGCTG	582
181	Qy	GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgLeuAsnGlyHis	200
583	Db	GAATCTCTGGGCTTCCAGCTCCGCGCGCTCCCAAGAACTGCGCCTGGCGCAACAATATGCCAC	642
201	Qy	SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr	220
643	Db	AGTGTGCACATGACCTTCCTCTGGGCTAGAGATGGCTCTGGGTTCGCGCGGGAGTAC	702
221	Qy	ArgAlaLeuGlnLeuHisIleuHisIleTtpGlyValaAlaGlyArgProGlySerGluHisThr	240
703	Db	CGGCGCTGTGCAGCTGCATCTGCATCGCGGGGCTGCGAGTCTGTCGGGCTCGAGCACT	762
241	Qy	ValGluGlyHisArgPheProAlaGluIleHisValValHisIleuSerThrAlaPheAla	260
763	Db	GTGAAGGCCACCGTTTCCCTGCGCGAGATCCACGTGTTCACTCAGCACCGCTTTGCC	822
261	Qy	ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu	280
823	Db	AGAGTTGACGAGGCTTTGGGCGCCCCGGGAGGCTTGGCGTGTGGCGGCTTTCTGGAG	882
281	Qy	GluGlyProGlnGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla	300
883	Db	GAGGGCCCGAAGAAACAAGTGGCTATAGAGCAGTGTCTGTCTCGCTTGAAGAAATCGCT	942
301	Qy	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp	320
943	Db	GAGNAGGCTCAGAGACTCAGGTCCACAGNCTGGACATATCTGCATCTCTGCCCTCTGAC	1002
321	Qy	PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal	340
1003	Db	TTCAGCGCTACTTCCAATATGAGGGGTCTCTGCATACACCGCCCTGTGCCAGGGGTGC	1062
341	Qy	IleTtrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer	360
1063	Db	ATCTGAGCTGTGTTTAACAGACAGTGATGCTGAGTGTCTAAGCAGCTCCACACCTCTCT	1122
361	Qy	AspThrLeuTrrPglyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro	380
1123	Db	GACACCTGTGGGGACCTGTGTGACTCTCGGCTACAGCTGAACCTTCGAGCGACGACGCT	1182
381	Qy	LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla	400
1183	Db	TTGAATGGGCGAGTGATGTAGGGCTCTCTTCCCTGCTGGAGTGGACAGCAGTCTCTGGGCT	1242
401	Qy	AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe	420
1243	Db	GCTGAGCCAGTCCAGCTGAATTCCTGCCCTGGCTGCTGGTGACATCTAGCCCTGGTTTTT	1302
421	Qy	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgGlnHisArg	440
1303	Db	GGCCTCCTTTTTGTGTCAACAGCGTCGGTTCCTTGTGCAGATGAGAAGGACAGCAGA	1362
441	Qy	ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla	459
1363	Db	AGGGGAACCAAGGGGGTGTGAGCTACCGCCACGAGAGGTAGCCGAGACTGGAGCC	1419

RESULT 14  
US-09-949  
; Sequenc





GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 17, 2006, 15:26:00 ; Search time 1362 Seconds  
(without alignments)  
2786.817 Million cell updates/sec

Title: US-09-967-237B-2

Perfect score: 2424

Sequence: 1 MAPLCSPWMLPLIPAPAG.....RRGTGGSVYRPAEVAETGA 459

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
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-MAXLEN=2000000000 -HOST=abs06p  
-USER=US0967237 @CGN 1.1 1549 @runat\_15022006\_182254\_28230 -NCPU=6 -ICPU=3  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA Main:

1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
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3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
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9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2424	100.0	1522	3	Sequence 1695, Ap
3	2424	100.0	1522	3	Sequence 1, Appli
4	2424	100.0	1522	7	US-09-967-237-1
5	2424	100.0	1522	7	US-10-723-795-1
6	2424	100.0	1522	8	US-10-795-933-5
7	2424	100.0	1522	8	US-10-888-694-1
	2424	100.0	1522	8	US-10-921-590-1

8	2424	100.0	1552	3	US-09-954-456-89	Sequence 89, Appl
9	2424	100.0	1552	3	US-09-954-456-726	Sequence 726, App
10	2424	100.0	1552	3	US-09-960-706-1080	Sequence 1080, Ap
11	2424	100.0	1552	3	US-09-873-367C-516	Sequence 516, App
12	2424	100.0	1552	3	US-09-968-007A-213	Sequence 213, App
13	2424	100.0	1552	6	US-10-301-822-11	Sequence 11, Appli
14	2424	100.0	1552	6	US-10-465-572-9	Sequence 9, Appli
15	2424	100.0	1552	6	US-10-172-118-574	Sequence 574, App
16	2424	100.0	1552	6	US-10-388-360-291	Sequence 291, App
17	2424	100.0	1552	6	US-10-295-027-305	Sequence 305, App
18	2424	100.0	1552	6	US-10-295-027-1022	Sequence 1022, Ap
19	2424	100.0	1552	7	US-10-342-887-574	Sequence 574, App
20	2424	100.0	1552	7	US-10-734-564-71	Sequence 71, Appl
21	2424	100.0	1552	8	US-10-723-860-460	Sequence 460, App
22	2424	100.0	1552	8	US-10-921-590-70	Sequence 70, Appl
23	2424	100.0	1552	9	US-10-848-755A-94	Sequence 94, Appl
24	2424	100.0	1552	9	US-10-843-641A-516	Sequence 516, App
25	2424	100.0	1552	9	US-10-843-641A-3116	Sequence 3116, App
26	2424	100.0	1552	9	US-10-843-641A-3753	Sequence 3753, Ap
27	2424	100.0	1552	9	US-10-843-641A-6683	Sequence 6683, Ap
28	2424	100.0	1552	9	US-10-794-514A-295	Sequence 295, App
29	2424	100.0	1552	9	US-10-756-149-474	Sequence 474, App
30	2424	100.0	1552	8	US-10-723-860-5135	Sequence 5135, Ap
31	2419	99.8	1833	3	US-09-783-708-2	Sequence 2, Appli
32	2416	99.7	1572	9	US-10-936-626-14	Sequence 14, Appl
33	2416	99.7	1572	9	US-10-938-061-14	Sequence 14, Appl
34	2233	92.1	5052	8	US-10-795-933-23	Sequence 23, Appl
35	2227	91.9	1399	8	US-10-795-933-1	Sequence 1, Appli
36	2058	84.9	1248	9	US-10-794-514A-321	Sequence 321, App
37	1938	80.0	1215	9	US-10-794-514A-323	Sequence 323, App
38	1596	65.8	1965	8	US-10-921-590-79	Sequence 79, Appl
39	1176.5	48.5	10898	3	US-09-772-719-5	Sequence 5, Appli
40	1176.5	48.5	10898	3	US-09-967-237-5	Sequence 5, Appli
41	1176.5	48.5	10898	7	US-10-723-795-3	Sequence 3, Appli
42	1176.5	48.5	10898	8	US-10-888-694-5	Sequence 5, Appli
43	1176.5	48.5	10898	8	US-10-921-590-3	Sequence 3, Appli
44	988	40.8	586	8	US-10-921-590-73	Sequence 73, Appl
45	714	29.5	415	3	US-09-772-719-28	Sequence 28, Appl

#### ALIGNMENTS

##### RESULT 1

US-10-102-524-1695  
; Sequence 1695, Application US/10102524  
; Publication No. US20030109434A1

GENERAL INFORMATION:  
; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; APPLICANT: Gaiger, Alexander

; APPLICANT: Gordon, Brian

; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF KIDNEY CANCER  
; FILE REFERENCE: 210121.572  
; CURRENT APPLICATION NUMBER: US/10102.524  
; CURRENT FILING DATE: 2002-03-19

; NUMBER OF SEQ ID NOS: 1863

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1695

; LENGTH: 1519

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-102-524-1695

Alignment Scores:

Pred. No.: 1.3e-227 Length: 1519  
Score: 2424.00 Matches: 459  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 5 Gaps: 0



US-09-967-237B-2 (1-459) x US-10-102-524-1695 (1-1519)

QY 1 MetAlaProLeuCysProSerProTTPLeuProLeuLeuIleProAlaProAlaProGly 20  
DB 10 ATGGCTCCCTGTGCCCCCAGCCCTGGCTCCCTCTGTGTGATCCGGCCCTGTCTCCAGGC 69  
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40  
DB 70 CTCACCTGTCAACTGCTGCTGTCACTGCTGCTTCTGATGCTGTCCATCCCCAGAGGTTG 129  
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60  
DB 130 CCCCAGATGACGAGGAGATCCCTTGGGAGGAGGCTTCTTGGGGAAGATGACCCACTG 189  
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80  
DB 190 GCGGAGGAGGATCTGCCCACTGAGAGGATTCACCCAGAGAGGAGGATCCACCCGAGAG 249  
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValHisPro 100  
DB 250 GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAATTAAGCCT 309  
QY 101 LysSerGluGluGlySerLeuLeuLeuLeuAspLeuProThrValGluAlaProGly 120  
DB 310 AAATCAGAAAGAGGCTCCCTGAGGTAGAGATCTACTACTGTGTAGGCTCTCTGGA 369  
QY 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
DB 370 GATCCTCAAGAACCCAGATATATGCCACAGGACAAAGAGGAGATGACACAGATCAT 429  
QY 141 TrpArgTyrGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160  
DB 430 TGGCGCTATGAGGCGACCCGCCCTGGCCCGGGTGTCCCGAGCTGCGCGGCGCGCTTC 489  
QY 161 GlnSerProValAspIleArgProGlnLeuAlaPheCysProAlaLeuArgProLeu 180  
DB 490 CAGTCCCGGTGATATCCCGCCCCAGCTCGCCGCTTCTGCCCCGCGCTTGGCCCCCTG 549  
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAnglyHis 200  
DB 550 GAACCTCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTGGCGCTCGGCAACATGGCCAC 609  
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220  
DB 610 AGTGTGCAACTGACCTGCTCTGCGCTAGAGATGGCTCTGGGTCGCCGGCGGAGTAC 669  
QY 221 ArgAlaLeuGlnLeuHisLeuHisTTPGlyValAlaGlyArgProGlySerGluHisThr 240  
DB 670 CCGGCTCTGACGCTGCATCTGCATCGGGGGCTGCAGGTGCTCGGGCTCGGAGCACAT 729  
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260  
DB 730 GTGGAAGGCCACCGTTCCTCCCGAGATCCACGTGTTCCACTCAGCACCGCTTTGCC 789  
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu 280  
DB 790 AGAGTTGACGAGGCTTTGGGGCGCCCGGAGGCTGGCCGCTGTGGCGGCTTTCTGGAG 849  
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluIleAla 300  
DB 850 GAGGCGCCGAAGAAACAGTGCCTATGACAGTTGCTGCTCGTTGGAAAGAAATCGCT 909  
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320  
DB 910 GAGGAAGCTCAGAGACTCAGTCCAGGACTGACATATCTGCACCTCTGCTGCTCTGAC 969  
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340  
DB 970 TTCAGCGCGCTACTTCCAATATGAGGGTCTCTGACTACACCGGCTGTGCGGAGGTGTC 1029  
QY 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
DB 1030 ATCTGGACTGTGTTTACCAGACAGTGAATGCTGAGTGTAAAGCAGCTTCCACACCTCTCT 1089

QY 361 AspThrLeuTTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380  
DB 1090 GACACCTGTGGGACACTGCTGACTCTGGCTACAGCTGAACCTTCGAGCGACGACGCT 1149  
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
DB 1150 TTGAATGGGCGAGTGATGAGGCTCTTCCCTGCTGGAGTGACAGCAGCTCTCGGCT 1209  
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
DB 1210 GCTAGCCAGTCCAGCTGAATCTCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1269  
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440  
DB 1270 GGCCTCCTTTTGTCTGCTCACCAGCTCGGCTTCTTGTGTCAGATGAGAGCGACAGCA 1329  
QY 441 ArgGlyThrIysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459  
DB 1330 AGGGGAACCAAGGGGCTGTGAGCTACCGCCAGCAGAGGTACCGGAGCTGGAGCC 1386

## RESULT 2

US-09-772-719-1  
; Sequence 1, Application US/09772719  
; Patent No. US20020137910A1  
; GENERAL INFORMATION:  
; APPLICANT: Zavada, Jan  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: MN Gene and Protein  
; NUMBER OF SEQUENCES: 86  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Leona L. Lauder  
; STREET: 369 Pine Street  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/772,719  
; FILING DATE: 30-JAN-2001  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/485,049  
; FILING DATE: 07-JUN-1995  
; APPLICATION NUMBER: US 08/260,190  
; FILING DATE: 15-JUN-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lauder, Leona L.  
; REGISTRATION NUMBER: 30,863  
; REFERENCE/DOCKET NUMBER: D-0021.3E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-981-2034  
; TELEFAX: 415-981-0332  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1522 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
US-09-772-719-1

Alignment Scores: 1 31e-227 Length: 1522  
Pred. No.: 2424.00 Matches: 459  
Score:



Db 133 CCCCGAGTGCAGGAGGANTCCCCCTTGGGAGGAGGCTCTTCTGGGGGAAGATGACCCCACTG 192  
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80  
Db 193 GCGGAGGAGGATCTGCCAGTGAAGAGATTCACCCAGAGGAGGATCCACCCGGAGAG 252  
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100  
Db 253 GAGGATCTACTGCGAGAGGAGGATCTACTCTGGAGGAGGATCTACTCTGAAGTTAAGCCT 312  
Qy 101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120  
Db 313 AAATCAGAGAAGAGGCTCCCTGAAGTTAGAGATCTACTCTGTGAGGCTCTCTGGA 372  
Qy 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
Db 373 GATCCTCAAGACCCAGAGATATGCCACAGGACAAAGAGGGGATGACCAAGTCAAT 432  
Qy 141 TrpArgTyrGlyGlyAspProTrpProArgValSerProAlaCysAlaGlyArgPhe 160  
Db 433 TGGCGCTATGGAGCGCACCCGCTGGCCCGGGGTGTCCCGAGCCTGCGCGGGCGGCTTC 492  
Qy 161 GluSerProValAspLeuArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180  
Db 493 CAGTCCCGGTGGATATCCGCGCCCACTCGCGCCCTTCTGCCCGGCCCTGGCGCCCTG 552  
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHis 200  
Db 553 GAACCTCTGGGCTTCAGCTCCCGCCCTCCAGAGCTGCGCTGCGCAACATGGCCAC 612  
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220  
Db 613 AGTGTGCAACTGACCTTCCTCTGGGTAGAGATGGCTCTGGTCCCGGGCGGAGTAC 672  
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThr 240  
Db 673 CGGCTCTGAGCTGCAATCTGCACTGGGGGGCTGCAAGTCTGTCGGGCTCGAGACACT 732  
Qy 241 ValGluGlyHisArgPheProAlaGluHisValValHisLeuSerThrAlaPheAla 260  
Db 733 GTGGAGGCCACCGTTTCCCTCCGAGATCCACGTGGTTCCACTCAGCACCGCCTTGGC 792  
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280  
Db 793 AGAGTTACAGGCGCTTGGGGCGCCCGGAGGCTGGCCGCTGTTGGCGGCTTTCTGGAG 852  
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluAla 300  
Db 853 GAGGGCCCGAAGAAACAGTGCCCTATGAGCAGTTGCTGTCTGCTTGGGAAGAAATCGCT 912  
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320  
Db 913 GAGGAGGCTCAGAGACTCAGTCCAGGACTGGACATATCTGCACCTCTGCCCTCTGAC 972  
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340  
Db 973 TTCAGCGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGTGCCCAGGGGTGC 1032  
Qy 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360  
Db 1033 ATCTGGAGCTGTGTTAAACAGACAGTATGCTAGTGTCTAAGCAGCTCTCCACCCCTCTCT 1092  
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380  
Db 1093 GACACCTGTGGGACCTGTGACTCTCTCGCTACAGCTGAATTCGAGGCGAGCGAGCCT 1152  
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
Db 1153 TTGAATGGGCGAGTGATTTGAGGCTCTCTCCCTGCTGGAGTGAGACAGCAGTCTCTCGGCT 1212  
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
Db 1213 GCTGAGCCAGTCCAGCTGAATTTCTGCTGGCTGCTGTGTGACATCTCTAGCCCTGGTTTTT 1272

## RESULT 4

US-10-723-795-1  
; Sequence 1, Application US/10723795  
; Publication No. US20040146955A1  
; GENERAL INFORMATION:  
; APPLICANT: Supuran, Claudiu  
; APPLICANT: Scozzafava, Andrea  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Pastorek, Jaromir  
; TITLE OF INVENTION: CA IX-SPECIFIC INHIBITORS  
; FILE REFERENCE: MST-2393 US  
; CURRENT APPLICATION NUMBER: US/10/723,795  
; CURRENT FILING DATE: 2003-11-26  
; PRIOR APPLICATION NUMBER: 60/429,089  
; PRIOR FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 60/489,473  
; PRIOR FILING DATE: 2003-07-22  
; PRIOR APPLICATION NUMBER: 60/515,140  
; PRIOR FILING DATE: 2003-10-28  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (13)..(1389)  
; FEATURE:  
; NAME/KEY: mat peptide  
; LOCATION: (124)..(1389)  
US-10-723-795-1

## Alignment Scores:

Pred. No.:	1,31e-227	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	7	Gaps:	0

US-09-967-237B-2 (1-459) x US-10-723-795-1 (1-1522)

Qy 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProAlaProGly 20  
Db 13 ATGGCTCCCTGTGCCCCAGCCCTCGCTCCCTCTGTGTATCCGGCCCTGTCTCCAGGC 72  
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40  
Db 73 CTCACCTGTGCAACTGCTGCTGTCTGCTGTCTGCTGTCTGCTGTCTGCTGTCTGCTGTG 132  
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60  
Db 133 CCCCGAGTGCAGGAGGATTTCCCTTTGGGAGGAGGCTCTTCTGGGAAGATGACCCACTG 192  
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80  
Db 193 GGCAGAGGAGATCTGCCAGTGAAGAGATTACCCAGAGAGAGGATTCACCCGGAGAG 252  
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100  
Db 253 GAGGATCTACTGAGAGGAGGATCTACCTGGAGAGGAGGATCTACTCTGAAGTTAAGCCT 312  
Qy 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120





Db 373 GATCCTCAAGAACCCAGATAATATGCCCACAGGACAAAGAGGGGATGACCAAGAGTCAT 432  
Qy 141 TTPArgTyrGlyGlyAspProTTPProArgValSerProAlaCyAlaGlyArgPhe 160  
Db 433 TGGCGCTATGAGCGACCCCGCCCTGCGCCCGGTGTCCCGAGCCTCGCGGGCGCGCTTC 492  
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCyAsProAlaLeuArgProLeu 180  
Db 493 CAGTCCCGGTGGATATCCGCCCCCAGCTGCGCCCTTCTGCGCGCCCTGCGCCCCCTG 552  
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnAnglyHis 200  
Db 553 GAATCTCTGGGCTCCAGCTCCCGCCCTCCAGAACTGGCCCTCGCGCCCTCGGAGCCAC 612  
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220  
Db 613 AGTGTGAACCTGACCTGCGCTCTGGGCTAGAGATGGCTCTGGGTCCCGGGCGGGAGTAC 672  
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTTPGlyAlaAlaGlyArgProGlySerGluHisThr 240  
Db 673 CGGCTCTGACGCTGCAATCTGCACTGGGGGCTGCAGGTGTCCGGGCTCGGACCACT 732  
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260  
Db 733 GTGGAAGCCACCGTTTCCCTCGCGGAGATCCACGTGGTTCACCTCAGCACCGCCTTTGCC 792  
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280  
Db 793 AGAGTTGACGAGGCTTTGGGGCGCGCGGAGGCTGGCGGTGGTGGCGCGCTTTCTGGAG 852  
Qy 281 GluGlyProGluGlnAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300  
Db 853 GAGGGCCCGGAAGAAACAGTGCCTATGAGCAGGTGTCTGCTCTGCTTGGAGAAATCGCT 912  
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320  
Db 913 GAGGAAGGCTCAGAGACTCAGTCCAGGAGTGCACATATCTGCACCTCGCCCTCTGAC 972  
Qy 321 PheSerArgTyrPheGlnTyrGlySerLeuThrThrProProCyAsAlaGlnGlyVal 340  
Db 973 TTCAGCGCTACTTCCAATATAGGGGTCTCTGACTACACCGCCCTGTGCGCAGGGTGTG 1032  
Qy 341 IleTTPThrValPheAsnGlnThrValMetLeuSerAlaGlyGlnLeuHisThrLeuSer 360  
Db 1033 ATCTGGAGTGTGTATACCAACAGACAGTGTATGAGTGTAAAGCAGCTCCACACCTCTCT 1092  
Qy 361 AspThrLeuTTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380  
Db 1093 GACACCTGTGGGACCTGTGTACTCTCGGTACAGCTGAATCTCCGAGCGACGACGCT 1152  
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400  
Db 1153 TTGAATGGCGAGTGTAGGGCTCTTCCCTGCTGGAGTGGACAGCAGTCTCTCGGGCT 1212  
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
Db 1213 GCTGAGCAGTCCAGCTGAAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272  
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440  
Db 1273 GGCTCTCTTTTGTGTGTACACAGGCTGCGTTCCTTGTGCGAGTGAAGAGCGACACAGA 1332  
Qy 441 ArgGlyThrIysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459  
Db 1333 AGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACTGGAGCC 1389

## RESULT 7

US-10-921-590-1

; Sequence 1, Application US/10921590

; Publication No. US20050031623A1

; GENERAL INFORMATION:

; APPLICANT: Pastorek, Jaromir

; APPLICANT: Zavada, Jan  
; APPLICANT: Ortova Gut, Marta  
; APPLICANT: Zatovicova, Miriam  
; APPLICANT: Pastorekova, Silvia  
; APPLICANT: Zavadova, Zuzanna  
; TITLE OF INVENTION: SOLUBLE FORM OF CARBONIC ANHYDRASE IX (8-CA IX), ASSAYS TO DETECT  
; TITLE OF INVENTION: 8-CA IX, CA IX'S COEXPRESSION WITH HER-2/neu/c-erbB-2 AND CA  
; FILE REFERENCE: IX-SPECIFIC MONOCLONAL ANTIBODIES TO NON-IMMUNODOMINANT EPITOPES  
; CURRENT APPLICATION NUMBER: US/10/921,590  
; CURRENT FILING DATE: 2004-08-19  
; PRIOR APPLICATION NUMBER: 60/358,824  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/383,068  
; PRIOR FILING DATE: 2002-05-23  
; PRIOR APPLICATION NUMBER: 60/431,499  
; PRIOR FILING DATE: 2002-12-05  
; PRIOR APPLICATION NUMBER: PCT/US03/05136  
; PRIOR FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: PCT/US03/05137  
; PRIOR FILING DATE: 2003-02-21  
; NUMBER OF SEQ ID NOS: 118  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1522  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (13)..(1389)  
; FEATURE:  
; NAME/KEY: mat peptide  
; LOCATION: (124)..(1389)  
US-10-921-590-1

## Alignment Scores:

Pred. No.: 1,31e-227 Length: 1522  
Score: 2424.00 Matches: 459  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 8 Gaps: 0

US-09-967-237B-2 (1-459) x US-10-921-590-1 (1-1522)

Qy 1 MetAlaProLeuCyAsProSerProTTPLeuProLeuLeuLeuProAlaProAlaProGly 20  
Db 13 ATGGCTCCCTGTGCCCCCAGCCCCCTGGCTCCCTGTGTGATCCGCGCCCTGTCTCCAGGC 72  
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40  
Db 73 CTACTGTGCACTGTGCTGTCTACTGCTGCTTCTGATGCTGTCCATCCCAGAGGTG 132  
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGlyAspAspProLeu 60  
Db 133 CCCGGATGCAGGAGGATCCCTTGGGAGGAGCTCTTCTGGGGAAGATGACCCACTG 192  
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80  
Db 193 GGGCAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGATCCACCCGAGAG 252  
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValIysPro 100  
Db 253 GAGGATCTACTGGAGGAGGAGGATCTACTTGGAGAGGAGGATCTACTTGAAGTTAAGCCT 312  
Qy 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120  
Db 313 AAATCAGAAGAAGAGGCTCCCTGAACTTAGAGGATCTACTACTGTTAGGCTCTCTGA 372  
Qy 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140  
Db 373 GATCCTCAAGAACCCAGAAATATATGCCAGGACAAAGAGGGGATGACCAAGTCAAT 432





Db 523 CAGTCCCGGTGGATATCCGCCCCAGCTCGCGCTTCTGCGCGGCTTGGCGCCCTG 582  
Qy 181 GluLeuLeuGlyPheGlnLeuProLeuProGlnLeuArgLeuArgLeuHis 200  
Db 583 GAACTCTGGGCTTCCAGCTCCGCGCGCTCCGAACTGGCGCTGGCGCAATGGCCAC 642  
Qy 201 SerValGlnLeuThrLeuProGlnLeuMetAlaLeuGlyProGlyArgGluTyr 220  
Db 643 AGTGTGCACTGACCTTGGCTTGGGCTAGAGATGGCTTGGGTCCCGGGGGAGTAC 702  
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaGlyArgProGlySerGluHisThr 240  
Db 703 CGGCTCTGCGAGCTGCACTGCGGGGCTGCGAGCTCGTCCGGCTCGGAGCACACT 762  
Qy 241 ValGluGlyHisArgPheProAlaGluLeuHisValValHisLeuSerThrAlaPheAla 260  
Db 763 GTGGAAGGCCACCGTTTCCCTGCGCGAGATCCAGTGGTTTCCACTCAGCACCGCTTTGCC 822  
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu 280  
Db 823 AGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTGGCGCTTGGCGGCTTCTTGGAG 882  
Qy 281 GluGlyProGluGlnAenSerAlaTyrGlnLeuLeuSerArgLeuGluLeuAla 300  
Db 883 GAGGCGCGGAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTGGAGAAATCGCT 942  
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspLeuSerAlaLeuLeuProSerAsp 320  
Db 943 GAGGAGGCTCAGAGACTCAGGTCAGGATCCAGGATGAGATATCTGCACCTCTGCTGAC 1002  
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrProProCysAlaGlnGlyVal 340  
Db 1003 TTGAGCGCGTACTTCCAAATAGAGGGTCTCTGACTACCGCGCTTGGCGGAGGTC 1062  
Qy 341 IleTrpThrValPheAenGlnThrValMetLeuSerAlaGlyGlnLeuHisThrLeuSer 360  
Db 1063 ATCTGGACTGTGTTAACAGAGACAGTGTGCTGAGTCTAAGCAGCTCCACACCTCTCT 1122  
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAenPheArgAlaThrGlnPro 380  
Db 1123 GACACCTGTGGGACCTGTGACTCTCGGCTACAGCTGAACCTTCCGAGGCGACGCT 1182  
Qy 381 LeuAenGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400  
Db 1183 TTGAATGGGCGAGTGTGAGGCTCTTCCCTGCTGGAGTGGACAGCTCTCGGCT 1242  
Qy 401 AlaGluProValGlnLeuAenSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420  
Db 1243 GCTGAGCCAGTCCAGCTGAATCTCTGCTGGCTGCTGCTGACATCTTAGCCCTGTTT 1302  
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440  
Db 1303 GGCCTCTTTTGTGTCCACAGCGTCCGCTTCTTCTGCTGGAGTGGACAGCTCCGAGCAGA 1362  
Qy 441 ArgGlyThrIysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459  
Db 1363 AGGGGAACCAAGGGGTGTGAGTACTCGCCAGCAGAGGTAGCCGAGACTGGAGCC 1419

RESULT 9  
US-09-954-456-726  
; Sequence 726, Application US/09954456  
; Patent No. US20020115057A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc  
; TITLE OF INVENTION: Sets  
; FILE REFERENCE: 689290-76  
; CURRENT APPLICATION NUMBER: US/09/954,456  
; PRIOR FILING DATE: 2001-09-18  
; PRIOR APPLICATION NUMBER: US/60/233,617  
; PRIOR FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: US/60/234,052

; PRIOR FILING DATE: 2000-09-20  
; PRIOR APPLICATION NUMBER: US/60/234,923  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,134  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: US/60/235,637  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,638  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US/60/235,711  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,720  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,840  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: US/60/235,863  
; PRIOR FILING DATE: 2000-09-27  
; NUMBER OF SEQ ID NOS: 2276  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 726  
; LENGTH: 1552  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-954-456-726

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Pred. No.: 2424.00 Matches: 459  
Score: 100.0% Conservatives: 0  
Percent Similarity: 100.0% Mismatches: 0  
Best Local Similarity: 100.0% Indels: 0  
Query Match: 100.0% Gaps: 0  
DB: 3

US-09-967-237B-2 (1-459) x US-09-954-456-726 (1-1552)

Qy 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuLeuProAlaProAlaProGly 20  
Db 43 ATGGCTCCCTGTGTGCCCGCCAGCCCTGGCTCCCTCTGTGTGATCCCGGCCCTGTCTCCAGGC 102  
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40  
Db 103 CTCACTGTGCACTGTGCTGTCTGATGCTCTGTGATGCTGTCTGATGCTGTCTGATGCTGT 162  
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60  
Db 163 CCCCGGATGAGGAGGATTCCTCCCTTGGGAGGAGGCTCTTCTGGGGAAGATGACCCACTG 222  
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80  
Db 223 GCGGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGAGGAGGATTCACCCCGGAGAG 282  
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLeuPro 100  
Db 283 GAGGATCTACCTGAGGAGGAGGATCTACCTGAGGAGGAGGATCTACCTGAGTGAAGCTT 342  
Qy 101 LysSerGluGluGlySerLeuLeuLeuLeuLeuLeuProThrValGluAlaProGly 120  
Db 343 AAATCAGAGAGAGGAGGCTCCCTGAGTTAGAGGATCTACTACTGTTGAGGCTCTCTGGA 402  
Qy 121 AspProGlnGluProGlnAenAlaHisArgAspIysGluGlyAspAspGlnSerHis 140  
Db 403 GATCCTCAAGAACCCCAAGATAATGCCACAGGACAAAGAGGAGGATGACACAGATCAT 462  
Qy 141 TrpArgTyrGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160  
Db 463 TGGCGCTATGAGGCGGACCCCGCTTGGCCCGGGGTGTCCTCCAGCTCGCGGGCGCTTC 522  
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180  
Db 523 CAGTCCCGGTGGATATCCGCCCCCAGCTGCGCGCTTCTGCGCGGCTTCTGCGGCCCCCTG 582  
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAenAsnGlyHis 200

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Db 583 GAACCTCTGGGCTTCCAGCTCCCGCCGCTCCAGAACTCGCGCTGCCCAACAATGGCCAC 642
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 643 AGTGTGCAACTGACCTTGCCTCTCTGGCTAGAGATGGCTCTGGTCCCGGGCGGAGTAC 702
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTTPGlyAlaGlyArgProGlySerGluHisThr 240
Db 703 CGGGCTCTGAGCTGCATCTGCATCGGGGGCTGTCAGTCTCTCGGGCTCGAGACACAT 762
Qy 241 ValGluGlyHisArgPheProAlaGluHisValHisValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGGTTTCACTCAGCACCGCTTTGCC 822
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 823 AGAGTTGACGAGGCTTGGGGCGCGCGGAGGCTGCGCTGTGGCGCGCTTCTTGAG 882
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuSerArgLeuGluGluHisAla 300
Db 883 GAGGGCCCGAAGAAACAGTGCTATGACAGTTGCTGTCTCGCTTGGGAAGAAATCGCT 942
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAGGCTCAGAGACTCAGTCCAGAGACTGGACATATCTGCATCTCTGCCCTCTGAC 1002
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 1003 TTCAGCGCTACTTCCAAATATGAGGGTCTCTGACTACACCGCCCTGTGCCAGGGTGC 1062
Qy 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaGlnLeuHisThrLeuSer 360
Db 1063 ATCTGGACTGTGTTTAAACACAGACAGTGTATGAGTGTCTAAGCAGCTCCACACCTCTCT 1122
Qy 361 AspThrLeuThrProGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCTGTGGGACCTGTGACTCTCGGCTACAGCTGAATCTCCGAGCGACGAGCCT 1182
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1183 TTGAATGGCGAGTGATGAGGCTCTCTCCCTGCTGGAGTGACAGCAGCTCTCGGGCT 1242
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1243 GCTGAGCCAGTCCAGCTGGAATCTCTGCTGGCTGCTGGTGACATCTCTAGCCCTGGT 1302
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCTCTCTTTTGTGTGCACACGGCTCGCTTCTTGTGCAGATGAGAGGCGACACAGA 1362
Qy 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1363 AGGGGAACCAAGGGGTGTGAGCTACCGCCAGCAGAGTACCGAGACTGGAGCC 1419

RESULT 10
US-09-960-706-1080
; Sequence 1080, Application US/09960706
; Publication No. US20030134280A1
; GENERAL INFORMATION:
; APPLICANT: Mungier, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR FILING DATE: 2000-08-07,2001-09-24
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1080
; LENGTH: 1552
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66839
US-09-960-706-1080
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Alignment Scores:
Pred. No.: 1,34e-227 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
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US-09-967-237B-2 (1-459) x US-09-960-706-1080 (1-1552)

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Qy 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProAlaProGly 20
Db 43 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTGTTGATCCCGGCCCTGTCTCCAGGC 102
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACTGTGCAACTGCTGTCTGCTCACTGCTCTCTGATGCTCTCCATCCCCAGAGTTG 162
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerClyGluAspAspProLeu 60
Db 163 CCCCAGATCGAGGAGATTCCTCCCTTTGGGAGGAGGCTCTTCTGGGGAAGATGACCCACTG 222
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 223 GGCAGAGAGATCTGCCAGTGNAGAGGATTCACCCAGAGAGAGGATCCACCCGAGAG 282
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
Db 283 GAGGATCTACCTGAGAGAGGATCTACCTGGAGAGGAGATCTACCTGAAGTTAAGCCT 342
Qy 101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 343 AAATCAGAGAAGAGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTTGAGGCTCTCTGGA 402
Qy 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGlyAspAspGlnSerHis 140
Db 403 GATCTCTCAGAACCCAGATAATGCCACAGGACAAAGAGGGGATGACACAGATCAT 462
Qy 141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGCGCTATGGAGCGACCGCCCTGGCCCGGGGTGTCCCCAGCCTGCGCGGGCGGCTTC 522
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 523 CAGTCCCCGGTGGATATCCGCCCCAGCTCGCCGCTTCTGCCCCGGCCCTGCGCCCCCTG 582
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHis 200
Db 583 GAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTCGCAACAATGGCCAC 642
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 643 AGTGTGCAACTGACCTTGCCTCTCTGGGCTAGAGATGGCTCTGGGCTCCCGGGCGGAGTAC 702
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTTPGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 703 CGGGCTCTGAGCTGCATCTGCACTCGGGGGCTGTCAGGTCGTCCGGGCTCGAGACACAT 762
Qy 241 ValGluGlyHisArgPheProAlaGluHisValHisValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAAGGCCACCGTTTCCCTGCGAGATCCACGTGGTTTCACTCAGCACCGCTTTGCC 822
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 823 AGAGTTGACGAGGCTTGGGGCGCGCGGAGGCTGCGCGGTGTGTCGCCCTTCTTGAG 882
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluHisAla 300
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Db 1063 ATCTGACTGTGTGTTAAACACAGAGTGTGCTGAGTGCTAAAGCAGCTCCACACCTCTCT 1122
Qy 361 AspThrLeuTTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCTGTGGGACCTGTGACTCTCGGTACAGCTGNACTTCGAGGCGAGCAGCCT 1182
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1183 TTGAATGGCGAGTGTGAGGCTCTCTTCCCTGCTGGAGTGACAGCAGTCTCGGGCT 1242
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaValPhe 420
Db 1243 GCTGAGCCAGTCCAGCTGAATCTCTGCTGGCTGCTGGTGACATCTAGCCCTGGGTTTTT 1302
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCTCTCTTTTGTCTGTCACAGCTGCGCTTCTTGTGCGAGATGAGAGGCGAGCAGAGA 1362
Qy 441 ArgGlyThrIysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1363 AGGGAAACAAAGGGGTGTGAGCTACCGCCAGCAGAGGTAGCCGAGACTGGAGCC 1419
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## RESULT 12

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US-09-968-007A-213
; Sequence 213, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
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; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968, 007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237, 172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237, 173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237, 278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237, 294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237, 295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237, 316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 213
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-968-007A-213
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Pred. No.: 1,34e-227 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 100.0% Indels: 0
DB: 3 Gaps: 0
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US-09-967-237B-2 (1-459) x US-09-968-007A-213 (1-1552)
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Qy 1 MetAlaProLeuLeuCysProSerProTTPLeuProLeuLeuIleProAlaProAlaProGly 20
Db 43 ATGCTCTCCCTGTGGCCCGCCCGCTGGCTCCCTCTGTTGATCCCGGCCCTGCTCCAGGC 102
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACTGTGCAACTGTGCTGTCTCACTGTCTCTGATGCTGTCCATCCCGAGAGGTTG 162
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspProLeu 60
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Db 163 CCCCGATGACGAGGATTTCCCTTTGGAGGAGGCTCTTCTGGGAAAGATGACCCACTG 222
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
Db 223 GCGGAGGAGGATCTGCCAGTGAAGGATTCAACCAGAGAGGAGGATCCACCCGAGAG 282
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValIysPro 100
Db 283 GAGGATCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAAGTTAAGCCT 342
Qy 101 LysSerGluGluGlySerLeuIysLeuGluAspLeuProThrValGluAlaProGly 120
Db 343 AAATCAGAAAGAGAGGCTCCCTGAAAGTTAGAGGATCTACCTACTGTTGAGGCTCTCGGA 402
Qy 121 AspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
Db 403 GATCTCAAGAACCCAGATATATGCCACACAGGACAAAGAGGGGATGACACAGACTCAT 462
Qy 141 TrpArgTyrGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGCGCTATGAGAGGCGACCCCGCTTGGCCCGGGTGTCCCCAGCCTGCGCGGCGCTTC 522
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 523 CAGTCCCCGGTGGATATCCGCCCCAGCTGCGCCCTTCTGCCGCGCTGCGCCCCCTG 582
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlnHis 200
Db 583 GAACTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGCGCTGCGCAACAATGSCCAG 642
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 643 AGTGTGCAACTGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCCGGCGGGAGTAC 702
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTTPGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 703 CGGGCTCTGCAGCTGCATCTGCACCTGGGGGGCTCGAGTCTGTCGGGCTCGGAGCACT 762
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAGGCGCACCGTTTCCCTCCGAGATCCACGTGTTTCACTCAGCACCGCTTTTGGC 822
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu 280
Db 823 AGAGTTGACAGAGGCTTGGGGCGCCCGGAGGCTTGGCGCTGTGTCGCCCTTTCTGGAG 882
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluIleAla 300
Db 883 GAGGGCCCCGAAAGAAACAGTGCCTATGAGCAGTTGCTGTCTGCTTGGAAAGAAATCGCT 942
Qy 301 GluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAAGGCTCAGAGACTCAGGTCCCGAGCTGGACATATCTGCATCTCTGCCCTCTGAC 1002
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 1003 TTCAAGCCGCTACTTCCCAATATGAGGGGCTCTCTGACTACACCGCCCTGTGCCAGGGTGC 1062
Qy 341 IleTTPThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
Db 1063 ATCTGCACTGTGTTTAAACAGACAGTATGCTGAGTGTCTAGCAGGTCTCCACACCTCTCT 1122
Qy 361 AspThrLeuTTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
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Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1183 TTGAATGGCGAGTGTGAGGCTCTTCCCTGCTGGAGTGGAGCAGCAGTCTCTCGGGCT 1242
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaValPhe 420
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 17, 2006, 15:32:07 ; Search time 518 Seconds  
(without alignments)  
1880.959 Million cell updates/sec

Title: US-09-967-237B-2

Perfect score: 2424

Sequence: 1 MAPLCPSPWLPPLIPAPAG.....RRRTKGVSYPRAEVAETGA 459

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7204252 seqs, 1061369211 residues

Total number of hits satisfying chosen parameters: 14408504

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPCL=0 -LOPEXT=0 -UNITS=bite -START=1 -END=1 -MATRIX=blomsum62  
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-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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-USER=US09967237 @CGN 1.1 335 @runat\_15022006\_182256\_28276 -NCPU=6 -ICPU=3  
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications NA New:  
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2: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2424	100.0	1552	12	US-11-186-284-11
3	568	23.4	1701	7	US-10-063-703-73
4	568	23.4	1701	12	US-11-102-240-73

5	542.5	22.4	2771	8	US-10-276-233A-21	Sequence 21, Appl	
6	542.5	22.4	2775	9	US-11-072-175-87	Sequence 87, Appl	
7	409	16.9	1428	12	US-11-000-688-633	Sequence 633, App	
8	378	15.6	833	8	US-10-055-877-17	Sequence 17, Appl	
9	377	15.6	828	8	US-10-055-877-15	Sequence 15, Appl	
c	10	362	14.9	1224	12	US-11-136-527-1116	Sequence 1116, Ap
	11	362	14.9	1224	12	US-11-136-527-5212	Sequence 5212, Ap
12	359.5	14.8	1264	9	US-11-177-506-5	Sequence 5, Appli	
13	357.5	14.7	2357	12	US-11-000-688-845	Sequence 845, App	
14	342	14.1	1201	12	US-11-136-527-3817	Sequence 3817, Ap	
15	336	13.9	1858	12	US-11-136-527-556	Sequence 556, App	
16	333	13.7	1266	12	US-11-136-527-2459	Sequence 2459, Ap	
17	332	13.7	5787	12	US-11-169-041-59	Sequence 59, Appl	
18	312	12.9	7872	12	US-11-136-527-2235	Sequence 2235, Ap	
c	19	306	12.6	9858	7	US-10-893-483-185	Sequence 185, App
	20	306	12.6	36259	7	US-10-893-483-186	Sequence 186, App
21	304.5	12.6	3091	12	US-11-097-728-3	Sequence 3, Appli	
22	304.5	12.6	7941	12	US-11-097-728-1	Sequence 1, Appli	
23	304.5	12.6	8058	12	US-11-097-728-5	Sequence 5, Appli	
24	300	12.4	1104	12	US-11-000-688-914	Sequence 914, App	
25	300	12.4	1104	12	US-11-054-281-19	Sequence 19, Appl	
26	277	11.4	2531	8	US-10-131-826A-33	Sequence 33, Appl	
27	273	11.3	1670	8	US-10-131-826A-325	Sequence 325, App	
28	245	10.1	756	8	US-10-467-657-275	Sequence 275, App	
29	245	10.1	756	8	US-10-467-657-4007	Sequence 4007, Ap	
30	244	10.1	1400	12	US-11-136-527-4652	Sequence 4652, Ap	
c	31	224	9.2	629	12	US-11-136-527-3573	Sequence 3573, Ap
	32	198	8.2	1396	7	US-10-530-240-1	Sequence 1, Appli
33	197	8.1	600	12	US-11-136-527-7669	Sequence 7669, Ap	
34	179	7.4	1968	12	US-11-136-527-2510	Sequence 2510, Ap	
35	170.5	7.0	2363	12	US-11-049-348-3	Sequence 3, Appli	
36	149	6.1	600	12	US-11-136-527-7913	Sequence 7913, Ap	
37	148	6.1	2251	8	US-10-750-185-62901	Sequence 62901, A	
38	148	6.1	2251	8	US-10-750-623-62901	Sequence 62901, A	
39	144.5	6.0	2403	7	US-10-649-457-4	Sequence 4, Appli	
c	40	143.5	5.9	4990	12	US-11-128-061-932	Sequence 932, App
	41	143.5	5.9	4990	12	US-11-128-049-932	Sequence 932, App
42	143	5.9	1897	8	US-10-775-169-236	Sequence 236, App	
c	43	142	5.9	775	12	US-11-136-527-1683	Sequence 1683, Ap
c	44	142	5.9	775	12	US-11-136-527-5779	Sequence 5779, Ap
c	45	142	5.9	168516	12	US-11-121-086-3	Sequence 3, Appli

#### ALIGNMENTS

RESULT 1  
US-11-112-944-19  
; Sequence 19, Application US/11112944  
; Publication No. US20050244872A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Cole  
; TITLE OF INVENTION: Breast Cancer Gene Expression Biomarkers  
; FILE REFERENCE: US-325-US  
; CURRENT APPLICATION NUMBER: US/11/112,944  
; CURRENT FILING DATE: 2005-04-22  
; PRIOR APPLICATION NUMBER: US 60/564,757  
; PRIOR FILING DATE: 2004-04-23  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 19  
; LENGTH: 1552  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-112-944-19

Alignment Scores:  
Pred. No.: 7.51e-154  
Score: 2424.00  
Length: 1552  
Matches: 459  
Percent Similarity: 100.0%  
Conservative: 0  
Best Local Similarity: 100.0%  
Mismatch: 0  
Query Match: 100.0%  
Indels: 0  
Gaps: 0  
DB:









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Db 788 CTGACACACACCCCTTGCACACCCCTGCTCTGGACAGCTTTTCCGAACCCCGTGCAA 847
Qy LeuSerAlaLysGlnLeuHisThrLeuSerAspThrLeuTrp-----Gly 365
Db 848 ATTTCCAGGAGCAGCTGCTGGCTTTGGACAGACCCCTGTACTGCACACATGGAGCAG 907
Qy ProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnProLeuAsnGlyArgVal 385
Db 908 CCTTCCCGCAGAGAAATGATCAACAACCTCCGGCAGGTCAGAAAGTTTCGATGAGAGCTG 967
Qy IleGluAlaSerPheProAlaGlyValAspSerSerProArgAlaAlaGluProValGln 405
Db 968 GTATACACCTCTCTCC-----CAA 988
Qy LeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPheGlyLeuLeuPheAla 425
Db 989 GTGCAAGCTGTACTCGCGCAGCAGTACTGGCATCATCTCTCACTGGCCCTGGCT 1048
Qy 426 -----ValThrSerValAlaPheLeuValGlnMetArgArgGln 438
Db 1049 GGCATTCTTGGCATCTGTATTGTGGTGGTGTCTCCATTGGCTTTTTCAGAGGAAGAGT 1108
Qy 439 HisArgArgGlyThrLysGlyValSerTyrArgProAlaGluValAlaGluThrGly 458
Db 1109 ATCAAAAAGGTGATAACAAGGGAGTCATTTAAGCCGCCACCAAGATGGAGACTGAG 1168
Qy 459 Ala 459
Db 1169 GCC 1171
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## RESULT 6

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US-11-072-175-87
; Sequence 87, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR
; FILE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
; FILE REFERENCES: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072,175
; PRIOR APPLICATION NUMBER: 2005-03-05
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648,593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 87
; LENGTH: 2775
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-072-175-87
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Alignment Scores:
Pred. No.: 3.01e-27 Length: 2775
Score: 542.50 Matches: 134
Percent Similarity: 47.2% Conservative: 46
Best Local Similarity: 35.2% Mismatches: 150
Query Match: 22.4% Indels: 51
DB: 9 Gaps: 11
```

US-09-967-237B-2 (1-459) x US-11-072-175-87 (1-2775)

```
Qy 114 ProThrValGluAlaProGlyAspProGlnGluProGlnAsnAlaHisArgAsp--- 132
Db 77 CCGGCACAGCCGCGCCCGCC-----CCGACAGAGCCCGAGATGCCCGCGCAGCCTG 133
Qy 133 -----LysGluGlyAspAspGln----- 138
Db 134 CACGCGCGCGCGTCTCTGCTGTATTAAGGAACACAGCTTCCAGCCGCGGCCCA 193
Qy 139 -----SerHisTrpArgTyr-----GlyGlyAspProProTrpProArgVal 152
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## RESULT 7

US-11-000-688-633





```
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (21)..(806)
US-10-055-877-17

Alignment Scores:
Pred. No.: 1.18e-16 Length: 833
Score: 378.00 Matches: 98
Percent Similarity: 51.1% Conservative: 41
Best Local Similarity: 36.0% Mismatches: 116
Query Match: 15.6% Indels: 17
DB: 8 Gaps: 8

US-09-967-237B-2 (1-459) x US-10-055-877-17 (1-833)

Qy 131 ArgAspLysGluGlyAspAspGlnSerHis-TripArgTyr-----GlyGlyAspPr 147
Db 5 CGAGGCTCAGTGGGATGTCGAGGCTCAGTGGGATACCGGAGCACAACGGTCTCTAT 64
Qy 147 oProTTPProArgValSerProAlaCysAlaGlyArgPheGlnSerProValAspLeAr 167
Db 65 TCACCTGAAGGAATTTTCCCTATTGTCTGTGTGTGATCAGCAATCTCCAATTGAGATTA 124
Qy 167 gProGlnLeuAlaAlaPheCysProAlaLeuArgProLeuGluLeuLeuGlyPheGlnLe 187
Db 125 AACCAAGAAGTGAATATGACTTCCCTCCGACCCACTTAGTATC-----AAGTA 175
Qy 187 uProProLeuProGluLeuArgLeuArgAsnGlyHisSerValGlnLeuThrLeuPr 207
Db 176 TGACCCAAAGCTCAGTAAATCATCAGCAACAGCGGCATTCCTTCAATGTGACTTTGA 235
Qy 207 oProGlyLeuGluMetAlaLeu-----GlyPro---GlyArgGluTyrArgAlaLe 223
Db 236 TGACACAGAGAACAATTCAGTCTCGTGGTGGTCTCTCACTGGAAAGCTACAGGTTACG 295
Qy 223 uGlnLeuHisLeuHisTTPGlyAlaAlaGlyArgProGlySerGluHisThrValGluGl 243
Db 296 GCAGGTTTCACTTCACTGGGGGTCGCTGTGTGATGACCGGCTCCAGCACAATAGTAGTGG 355
Qy 243 yHisArgPheProAlaGluLeuHisValHisLeu---SerThrAlaPheAlaArgVa 262
Db 356 AGTGAGCTATGTCGACAGCTCCATGTTGTTCACTGGAATTCAGACAAATACCCAGCTT 415
Qy 262 lAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGluGl 282
Db 416 TGTGAGGCGAGCTCATGAACAGATGAGCTGGCTGTCTTGGAGTGTGTTTACAGATTGG 475
Qy 282 yProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluLeuAlaGluGl 302
Db 476 T---GAACCTAATTCACCACTGCAAAAGATTACTGACACTTTGGATTCCATTAAAGAAA 532
Qy 302 uGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAspPheSe 322
Db 533 GGGTAAACAAACTCGAATTCACAAATTTTGACCTATTGTCTCTGCTTCCACCATCCTGGGA 592
Qy 322 xArgTyrPheGlnTyrGluGlySerLeuThrProProCysAlaGlnGlyValIleTr 342
Db 593 C---TACTGACATATCTCGTCTCTTACAGTTCCACCTCTTCTTGGAGAGTGTCAATG 649
Qy 342 pThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeu-----HisThrLe 359
Db 650 GATTGTTTAAAGCAACCTATAACATCAGCTCTCAACAGCTGGCCAAATTCGCAGTCT 709
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Qy 359 userAspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGl 379
Db 710 CCTGTGCACAGCGGAGGTGAAGCAGCAGCTTTTCTGTGAGCAATCAGCGCCACCACA 769
Qy 379 nProLeuAsnGlyArgValIleGluAlaSerPhe 390
Db 770 GCCTCTAAAGGCGCCAAAGTGAGAGCCTCTTTTC 803
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## RESULT 9

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US-10-055-877-15
; Sequence 15, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Verniet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; PRIOR FILING DATE: 2001-03-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 828
; TYPE: DNA
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ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (16)..(801)  
US-10-055-877-15

## Alignment Scores:

Pred. No.: 1.37e-16 Length: 828  
Score: 377.00 Matches: 95  
Percent Similarity: 51.3% Conservative: 39  
Best Local Similarity: 36.4% Mismatches: 111  
Query Match: 15.6% Indels: 16  
DB: 8 Gaps: 8

US-09-967-237B-2 (1-459) x US-10-055-877-15 (1-828)

```
Qy 141 TrpArgTyr-----GlyGlyAspProProTrpProArgValSerProAlaCysAla 157
Db 31 TGGGGATACCGGAGCACAACGGTCTTATTCACCTGGAAGGAATTTTCCCTTATGCTGAT 90

Qy 158 GlyArgPheGlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeu 177
Db 91 GGTGATCAGCAATCTCCAATTGAGATTAAACCAAGAGGTGAAATATGACTCTTCCCTC 150

Qy 178 ArgProLeuGluLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsn 197
Db 151 CGACACCTTAGTATC-----AAGTATGACCAAGCTCAGCTAAATCATCAGCAAC 201

Qy 198 AsnGlyHisSerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeu----- 214
Db 202 AGCGCCCATCTCTCAATGTTGACTTTGATCAGACAGAGAAACAAATCAGTCTCGGTGT 261

Qy 215 GlyPro---GlyArgGluTyrArgAlaLeuGlnLeuHisLeuHisLeuTrpGlyAlaAlaGly 233
Db 262 GGTCTCTCTCACTGGAAGCTACAGGTATGCGGAGGTTCACCTTCACTGGGGTCCGCTGAT 321

Qy 234 ArgProGlySerGluHisThrValGluGlyHisArgPheProAlaGluIleHisValVal 253
Db 322 GACCAGGCTCCGAGCACAATGATGAGTATGATGAGTATGCTGAGAGCTCCATGTTGTT 381

Qy 254 HisLeu---SerThrAlaPheAlaArgValAspGluAlaLeuGlyArgProGlyGlyLeu 272
Db 382 CACTGGAATTCAGACAAATACCCAGCTTTGTTGAGGAGCTCATGAACAGATGAGCTG 441

Qy 273 AlaValLeuAlaAlaPheLeuGluGluGlyProGluGluAsnSerAlaTyrGluGlnLeu 292
Db 442 GCTGTCTTGGGAGTGTGTTTACAGGTGGGT---GAACCTAATTCCTCAACCTGCAAAAGATT 498

Qy 293 LeuSerArgLeuGluGluIleAlaGluGluGlySerGluThrGlnValProGlyLeuAsp 312
Db 499 ACTGACACTTGGATTTCATTAAAGAAAGGTTAAACAACTCGATTTCACAAATTTGAC 558

Qy 313 IleSerAlaLeuLeuProSerAspPheSerArgTyrPheGlnTyrGluGlySerLeuThr 332
Db 559 CTATTGTCTCTGCTTCCACCATCTCGGAC---TACTGGACATATCTCGGTCTCTTACA 615

Qy 333 ThrProProCysAlaGlnGlyValIleTrpThrValPheAsnGlnThrValMetLeuSer 352
Db 616 GTTCCACCTCTTCTTGAGAGTGCACATGGATTGTTTAAAGCAACCTTATAAATCATCAGC 675

Qy 353 AlaLysGlnLeu-----HisThrLeuSerAspThrLeuTrpGlyProGlyAspSer 369
Db 676 TCTCAACAGCTGGCCAAATTCGAGCTCTCTGTGACAGCGGAGGTGAAGCAGCAGCT 735

Qy 370 ArgLeuGlnLeuAsnPheArgAlaThrGlnProLeuAsnGlyArgValIleGluAlaSer 389
Db 736 TTTCTGTGTGAGCAATCACCGCCCAACCAAGCTCTTAAAGGGCCGCAAAAGTGAGAGCTCT 795

Qy 390 Phe 390
Db 796 TTC 798
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RESULT 10

US-11-136-527-1116/c  
Sequence 1116, Application US/11136527  
Publication No. US20050287570A1  
GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Mounts, William M  
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
FILE REFERENCE: 031896-041000 (AM101086)  
CURRENT APPLICATION NUMBER: US/11/136,527  
CURRENT FILING DATE: 2005-05-25  
PRIOR APPLICATION NUMBER: US 60/574,294  
PRIOR FILING DATE: 2005-05-26  
NUMBER OF SEQ ID NOS: 362830  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 1116  
LENGTH: 1224  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-11-136-527-1116

Alignment Scores:  
Pred. No.: 1.96e-15 Length: 1224  
Score: 362.00 Matches: 105  
Percent Similarity: 49.2% Conservative: 56  
Best Local Similarity: 32.1% Mismatches: 112  
Query Match: 14.9% Indels: 54  
DB: 11 Gaps: 11

US-09-967-237B-2 (1-459) x US-11-136-527-1116 (1-1224)

```
Qy 166 IleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeuGluLeuLeuGlyPhe 185
Db 1200 ATAGGACCC---CTCGTGTGTGGATGTCGCTGCTCC-----AAATTACGTGTGTG 1150

Qy 186 GlnLeuProLeuProGluLeu-ArgLeuArgAsnAsnGlyHisSerValGlnLeuTh 205
Db 1149 CAG-----GGACTGTGAAGTCCACCAAGCATGGACACACCATTCAGTCAT 1105

Qy 205 rLeuProProGlyLeuGluMetAlaLeuGlyPro-----GlyArgGluTyrArgAl 222
Db 1104 CCTGAAGTCGAATCAGTTTGTTCAGGAGGACCCCTGCTCCTCAGGAGGAGGTGTA 1045

Qy 222 aLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGluHisThrValG 242
Db 1044 GTATGAAGTATAGATTTCTACTGGGAGACAGAGAAACACGCTGTTCTGACGACACG 985

Qy 242 uGlyHisArgPheProAlaGluIleHisValValHisLeu---SerThrAlaPheAla 261
Db 984 TTTCAAGCCCTTCCCATGGAGCTCCACCTGATCCACTGGAATTCACGCTGTTTGGCAG 925

Qy 261 gValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 281
Db 924 CATCGATGAGCGGTGGGAAACMCSASGGGATTTGTCATCATTCGCTGTTCTGTCAGAT 865

Qy 281 uGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluIleAlaG 301
Db 864 AGGG---AAGGAGCATTTGCTTGAAGGCTGTGACTGAGATCTTCAGGATATCCAATA 808

Qy 301 uGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 321
Db 807 CAAGGGAAAAATCCAAAAACAATTCATGCTTTAATCTTAACACATTTATTACCAACG 748

Qy 321 eSerArg---TyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVa 340
Db 747 TCTGCGGATTTACTGGGTCTATGAAGGATCTCTTACTATTTCACCTTGAGTGAAGGAG 688

Qy 340 lIleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeu----- 356
Db 687 TACTGTGATATTATTCGATACCCATTAATATATATCCAGCTGCAGATAGAAGATTTTCG 628

Qy 357 -----HisThrLeuSerAspThrLeuTrpGlyProGlyAspSerArgLeuG 372
Db 627 AAGACTGAGGACACATGTTAAGGGGGCAGAACTGTGCAAGGCTGTGACGGGATTTTGGG 568
```

```

Qy 372 nLeuAsnPheArgAlaThrGlnProLeuAenGlyArgValIleGluAlaSerPhe----- 390
Db 567 AGATAATTTCCGACCTACCCAGCCCTGAGTGACAGAGTATCCGAGCAGCAATTTTCAGTA 508
Qy 391 -ProAlaGlyValAspSerPro----- 398
Db 507 GCCAGAGAAACCTGAAACAAGCCCATTTGCATCAGGGAAGACGTTGGTCTCACAGAG 448
Qy 399 -----ArgAlaAlaGlu-ProValGlnLeuAsnSerCysAl 410
Db 447 TCCTTTGATCAGGAGTGGAACTCTCGACGCGGAGCTTCCTGTTAACTTCAAGCCCTGCA 388
Qy 410 euAla-----AlaGlyAspIleLeuAlaLeu-ValPheGlyLeuLeu 423
Db 387 TTATCTTCAGTTACTGGCGCTTTGATGGAGATCTGTGRCATTTGTCTGTATACATGWTGT 328
Qy 424 PheAlaValThrSerValAla-PheLeuValGlnMetArgArgGlnHisArgArgGlyTh 443
Db 327 TATGAGATATTAGAAAGTGGCTGTTCACTATAAAGAAATCAGTGTGTCATGCACACMCCAC 268
Qy 443 rLysGlyGlyVal 447
Db 267 AGCTTCTGGAATT 255

RESULT 11
US-11-136-527-5212
; Sequence 5212, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; TITLE OF INVENTION: Mounts, William M
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5212
; LENGTH: 1224
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-5212

Alignment Scores:
Pred. No.: 1.96e-15 Length: 1224
Score: 362.00 Matches: 105
Percent Similarity: 49.2% Conservative: 56
Best Local Similarity: 32.1% Mismatches: 112
Query Match: 14.9% Indels: 54
DB: 12 Gaps: 11

US-09-967-237B-2 (1-459) x US-11-136-527-5212 (1-1224)

Qy 166 IleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeuGluLeuLeuGlyPhe 185
Db 25 ATAGGACCC---CTCGCTGTGGATGTCGCTCTCC-----AAATTACGTGGTGTG 75
Qy 186 GlnLeuProProLeuProGluLeu-ArgLeuArgAsnAsnGlyHisSerValGlnLeuTh 205
Db 76 CAG-----GGAGTGTGAAGTCCACCAGATGGACACACCACTTCAAGTCAT 120
Qy 205 rLeuProProGlyLeuGluMetAlaLeuGlyPro-----GlyArgGluTyArgAl 222
Db 121 CCTGAAGTCGAATCAGATTGTCAGGAGACCGCTCCCTCAGGACGAGGAGTTGTAAGT 180
Qy 222 aLeuGlnLeuHisLeuHisThrGlyAlaAlaGlyArgProGlySerGluHisThrValG1 242
Db 181 GTATGAAGTTAGATTTCACCTGGGGAGAGAAACACGCGTGGTCTCTGAGCACACGGTCAA 240
Qy 242 uGlyHisArgPheProAlaGluIleHisValHisLeu---SerThrAlaPheAlaAr 261

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Db 241 TTTCAAAGCCTTCCCATGAGCTCCACCTGATCCCAATTCACGCTGTTGGCAG 300
Qy 261 gValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGluG1 281
Db 301 CATCGATAGCGGTTGGGAAACMCASGCGCATTTGCATCATTTGCATGTTCTGCTCCAGAT 360
Qy 281 uGlyProGluGluAsnSerAlaTyrgluGlnLeuLeuSerArgLeuGluIleAlaG1 301
Db 361 AGGG---AAGGAGCATGTTGGCTTGAAGCGTGTGACTGAGATATCTTCAGGATATCCAATA 417
Qy 301 uGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAspPh 321
Db 418 CAAGGGAAATCCAAACAAATTCATGCTTTAATCTTAACACTTTATTACAGACCCCTCT 477
Qy 321 eSerArg---TyPheGlnTyrgluGlySerLeuThrProProCysAlaGlnGlyVa 340
Db 478 TCTGCGGGATTACTGGGTCTATGAGAGATCTCTTACTATTCCACCTTGCAGTGAAGGAGT 537
Qy 340 lIleThrThrPheAsnGlnThrValMetLeuSerAlaLysGlnLeu----- 356
Db 538 TACCTGGATATTATCCGATACCCATTAACTATATCCAGCTGCAGATAGAGAATTTTCG 597
Qy 357 -----HisThrLeuSerAspThrLeuTpGlyProGlyAspSerArgLeuG1 372
Db 598 AAGACTGAGGACACATGTTAAGGGGCGACAACTYGTGCAAGGCTGTGACGGGATTTTGGG 657
Qy 372 nLeuAsnPheArgAlaThrGlnProLeuAsnGlyArgValIleGluAlaSerPhe----- 390
Db 658 AGATAATTTCCGACCTACCCAGCCCTTGAGTGACAGAGTATCCGAGCAGCAATTTTCAGTA 717
Qy 391 -ProAlaGlyValAspSerPro----- 398
Db 718 GCCAGAGAAACCTGAAACAAGCCCATYTGTCATCAGGGAAGACGTTGGTCTYCACAGAG 777
Qy 399 -----ArgAlaAlaGlu-ProValGlnLeuAsnSerCysAl 410
Db 778 TCCTTTGATGAGGAGTGGAAACTCTTWAGCGCGGAGCTTCTGTGTAACTTCAAGCCCTGCA 837
Qy 410 euAla-----AlaGlyAspIleLeuAlaLeu-ValPheGlyLeuLeu 423
Db 838 TTATCTTCAGTTACTGGCGCTTTGATGGAGATCTGTGRCATTTGTGTATACATGWTGT 897
Qy 424 PheAlaValThrSerValAla-PheLeuValGlnMetArgArgGlnHisArgArgGlyTh 443
Db 898 TATGAGATATTAGAGTGGCTGTTCACTATAAAGAAATCAGTGTGTCATGCACACMCCAC 957
Qy 443 rLysGlyGlyVal 447
Db 958 AGCTTCTGGAATT 970

RESULT 12
US-11-177-506-5
; Sequence 5, Application US/11177506
; Publication No. US20060029956A1
; GENERAL INFORMATION:
; APPLICANT: Beyer, Wayne F.
; APPLICANT: Venetta, Thomas M.
; APPLICANT: Groelke, John W.
; APPLICANT: Blaesius, Rainer H.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; FILE REFERENCE: 46143/294851
; CURRENT APPLICATION NUMBER: US/11/177,506
; PRIOR FILING DATE: 2005-07-08
; PRIOR FILING DATE: 2004-07-09
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1264
; TYPE: DNA
; ORGANISM: Homo sapiens

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[illegible]

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Qy 144 -GlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPheGlnSerPr 163
Db 713 CAACGGCTCTGACCACTGGATGAACCTTTTCCCAAATGCCAAGGGGGAACCAAGTCGCC 772
Qy 163 oValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeuGluLeuLe 183
Db 773 CGTTGAGCTGCATACACTAAGACATCAGCGATGACCTTCTCTGAGCCATGGTCTGTGG-- 830
Qy 183 uGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHisSerValG1 203
Db 831 -----TCATTATGATGGTGGCTCTGCGCAAGACCATCTCGAATAATGGGAAGACCTGCCG 883
Qy 203 nLeuThrLeuProProGlyLeuGluMetAlaLeu-----GlyPr 216
Db 884 AGTTGTATTTGATGATACCTTATGATAGTCAATGCTGAGAGGGGGTCTCTCCCTGGACC 943
Qy 216 oGlyArgGluTyArgAlaLeuGlnLeuHisHisTrpGlyValAlaAlaGlyArgProG1 236
Db 944 C-----TACCGACTTCGCCAGTTTCACTTCCTGAGGGGCTCTTCGGATGATCATGG 994
Qy 236 ySerGluHisThrValGluGlyHisArgPheProAlaGluIleHisValHisLeuSe 256
Db 995 CTCTGAGCACACCGTGGATGAGTCAAGTATGCGAGCGGAGCTTCATTGGTTCACCTGGAA 1054
Qy 256 rThrAlaPheAlaArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValleuAl 276
Db 1055 CCGAAGTATAACACTTTTAAAGAAGCCCTTGAAGCAGCGCGATGGGATCGCTGTGATTGG 1114
Qy 276 aAlaPheLeuGluGluGlyProGluLeuAsnSerAlaTyArgLeuGlnLeuLeuSerArgLe 296
Db 1115 CATTTTCTGAAGATAGGA---CATGAGATGGGAGTTCCAGATTTTCTTGTATGATG 1171
Qy 296 uGluGluIleAlaGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLe 316
Db 1172 GGACAAGATTAAAGACAAGGCGAAGGAGCGCCCTTCCAAAGTTTGACCATCTGCGCT 1231
Qy 316 uLeuProSerAspPheSerArgTyPheGlnTyArgGlySerLeuThrThrProProCy 336
Db 1232 GTTCCCGGCA---TGCCGGGACTACTGAGACTTACCGAGGGCTCATTCACACGCGCGCCCTG 1288
Qy 336 sAlaGlnGlyValIleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLe 356
Db 1289 CGAGGAATGATGTGTGGCTGTCTGCTGAAGAGGCCCATACCGTGAGCTCTGACACAGAT 1348
Qy 356 uHisThrLeuSerAspThrLeuTrpGlyProGlyAspSer-----ArgLeuGlnLe 373
Db 1349 GGCCAAGCTGGGAGCCCTCTCTCCAGTGTGTGAGAACGAGCCGCCAGTGGCTCTTGTGAG 1408
Qy 373 uAsnPheArgAlaThrGlnProLeuAsnGlyArgValIleGluAlaSerPhe----- 390
Db 1409 CAATGGCGACCTTCCACAGCCTATCAATAACAGGGTGTGTGAGAGCTTCTTCAATGAGG 1468
Qy 391 -----ProAlaGlyValAspSer----- 396
Db 1469 CTGCTGGATCTTGGCCCTTTCAGGAAGGAACCTACCATTTGGAGAGCTTGGTTCCTTGC 1528
Qy 396 ----- 396
Db 1529 CTCCTTCTGTGTCTTCTTACCTCAAGTCTATTTCATTTTCCACACTGAGCAATGAATGTG 1588
Qy 397 -----SerProArgAlaAlaGluProValGlnLeuAsnSerCysLeuAlaAlaG1 413
Db 1589 AGAGATGTGTGTCAACAGATCTAAGTTACTTGTGTGAAGAAAGTACTTTCGACAAGATC 1648
Qy 413 yAspIleLeuAla-----LeuValPheGlyLeuLeuPheAlaValThrSerVa 429
Db 1649 TAATATGAAGCATAGATTTCACATTTGATCTCTGTAATATCATCTTCTTATATAAAGT 1708
Qy 429 lAlaPheLeuValGlnMetArgArgGlnHisArgArg 441
Db 1709 AGCATTTTGTGAAGTTTCAAGAGAAGAAACAGA 1745
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US-11-136-527-3817
; Sequence 3817, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3817
; LENGTH: 1201
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3817

Alignment Scores:
Pred. No.: 4.25e-14 Length: 1201
Score: 342.00 Matches: 93
Percent Similarity: 48.2% Conservative: 38
Best Local Similarity: 34.2% Mismatches: 113
Query Match: 14.1% Indels: 28
DB: 12 Gaps: 10

US-09-967-237B-2 (1-459) x US-11-136-527-3817 (1-1201)

Qy 140 HisTrpArgTyR-----GlyGlyAspProPro 148
Db 106 CACTGGCGCTTCAGCATCTTACGAGAGAAACACAGCAACTGTGCGCGCCCTCTC 165
Qy 149 Trp-----ProArgValSerProAlaCysAlaGlyArgPheGlnSerProValAspIle 166
Db 166 TGACCTGGCCCATGTCTCTACCG-----GGAGGCACCCAGCAGCTCTCCATTATATC 219
Qy 167 ArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeuGluLeuGlyPheGln 186
Db 220 CAGTGGACGATAGTGTCTATGACCCGACCGCTCAGGGTC-----TCC 270
Qy 187 LeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHisSerValGlnLeuThrLeu 206
Db 271 TATGATGTGCTGCTCTGAGATACCTCTGGAACACTGGTATTCTTCTCCAGGTGGAGTTT 330
Qy 207 ProProGlyLeuGlu-----MetAlaLeuGlyPro---GlyArgGluTyArgAla 222
Db 331 GACGATTCCTGTGAGGAGTCAGGGATCAGTGGTGGGCTCTGGGAACCACTACAGGCTG 390
Qy 223 LeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGlnHisThrValGlu 242
Db 391 AAGCAGTTTCACTTCCACTGGGAGCAACAGATGAATGGGCTCTGAGCACATGGTGGAC 450
Qy 243 GlyHisArgPheProAlaGluIleHisValValHisLeu---SerThrAlaPheAlaArg 261
Db 451 GGCCATGCTTACCCGCTGAGCTCCATTTGGTTCTCTGGAATTCATGAATATGAANAAT 510
Qy 262 ValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGluGlu 281
Db 511 TACAAGNAGCCACACCGGGGAGAGATGGATCGCGGTGATTGGAGTGTCTTCTGAAGCTC 570
Qy 282 GlyProGluGluAsnSerAlaTyArgGlnLeuLeuSerArgLeuGluGluIleAlaGlu 301
Db 571 GGG---GCCCATCAGAGGCCCTGCGAGAGGCTGTGGACATCTTGGCGGAAGTAAGACAC 627
Qy 302 GluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAspPhe 321
Db 628 AAGAACACACAGGTGACCATGGGGGCCCTTTGACCTCTTCTGCTGCTGCTGCTGCTGCTG 684
Qy 322 SerArgTyRPhenTyArgGlySerLeuThrThrProProCysAlaGlnGlyValIle 341
Db 685 CGGGATTACTGGACCTACCTGGCTCCCTCACCACCCCACTGCTGGCTGAGTCAGTCACC 744
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Qy 342 TrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSerAsp 361  
 Db 745 TGGATTGCAAGATGCCATTCAGGTGTCCTCCGAGCGAGCTGTCCACATTCGACACA 804  
 Qy 362 ThrLeuTrp-----GlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThr 378  
 Db 805 CTCTTGTTCTCCGGCGAGGTGAGGACGAGGAGGTGATGGTGAACAACCTTCGCGCCGCTC 864  
 Qy 379 GlnProLeuAsnGlyArgValIleGluAlaSerPhe 390  
 Db 865 CAACCACTACGGGCGCGCAACGTTTCGCTCCTTC 900

# RESULT 15

US-11-136-527-556  
 ; Sequence 556, Application US/11136527  
 ; Publication No. US20050287570A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wyeth  
 ; APPLICANT: Mounts, William M  
 ; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
 ; FILE REFERENCE: 031896-041000 (AM101086)  
 ; CURRENT APPLICATION NUMBER: US/11/136,527  
 ; CURRENT FILING DATE: 2005-05-25  
 ; PRIOR APPLICATION NUMBER: US 60/574,294  
 ; PRIOR FILING DATE: 2005-05-26  
 ; NUMBER OF SEQ ID NOS: 362830  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 556  
 ; LENGTH: 1858  
 ; TYPE: DNA  
 ; ORGANISM: Rattus norvegicus  
 US-11-136-527-556

Alignment Scores:  
 Pred. No.: 1.57e-13 Length: 1858  
 Score: 336.00 Matches: 98  
 Percent Similarity: 48.8% Conservative: 60  
 Best Local Similarity: 30.2% Mismatches: 142  
 Query Match: 13.9% Indels: 24  
 DB: 12 Gaps: 11

US-09-967-237B-2 (1-459) x US-11-136-527-556 (1-1858)

Qy 101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaPro--- 119  
 Db 70 AGAAAGAGAGACGACGACGTCAGATGAACCGCAGTGCCTTTTGACATGATCTAACCCAGAA 129  
 Qy 120 ---GlyAspProGlnGluProGlnAsnAlaHisArgAspLysGluGlyAspAspGln 138  
 Db 130 GCAGGAGCTGTCCAGCGCTGAGACACAGGAAAGCCATGGCTAAGGAGTGGGGTTAGGSC 189  
 Qy 139 SerHisTrpArgTyrGlyAspProProTrpProArgValSerProAlaCysAlaGly 158  
 Db 190 AGCCAC-----AATGGYCTTCGACGACCTGGCATGAACCTTTATCCAATTTGCCAAAGGG 240  
 Qy 159 ArgPheGlnSerProValAspIleArgProGlnLeuAlaPheCysProAlaLeuArg 178  
 Db 241 GACAAACCACTACCCATTTGAATGTCATCACTAAGACATCAGGCATGATCTCTCTGCAG 300  
 Qy 179 ProLeuGluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsn 198  
 Db 301 CCTTGGTCAGTA-----TCTTATGATCCTGGCTCTGTAAAGACCATCTCTGACACAT 351  
 Qy 199 GlyHisSerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeu-----Gly 215  
 Db 352 GCGAAGACCTCGACAGATTGTTTGTATGATACATACATTCGAYAGGTCCATGCTGAGAGGTGGS 411  
 Qy 216 Pro---GlyArgGluTyrArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArg 234  
 Db 412 CCTCTCTGTGACCTACCGCACTTCGCGARTTCATCTTCACTGGGGCTCCTCGGATGAC 471  
 Qy 235 ProGlySerGluHisThrValGluGlyHisArgPheProAlaGluIleHisValHis 254

Db 472 CATGGCTCTGAGCACACAGTGGATGGATGAAGTATGCTGCTGAGCTTCACCTGGTTAC 531  
 Qy 255 LeuSerThrAlaPhe-AlaArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaVa 274  
 Db 532 TGAACCCGAGATATAACACCTTCGGAGGAGGCTCTGAAGCAGCCGATGGATTGCTGT 591  
 Qy 274 LLeuAlaAlaPheLeuGluGlyProGluGluAsnSerAlaTyrGlnLeuLeuSe 294  
 Db 592 GGTGGCATTTTCTGAAGATAGGA---CGGAGAAAGGGCAGTTCARATTCCTCTGA 648  
 Qy 294 rArgLeuGluGluIleAlaGluGlySerGluThrGlnValProGlyLeuAspIleSe 314  
 Db 649 TGCCTGGACAAAATTAAGACTAAGGGCAAGGAGCTCTTTTAAATCACTTCGACCATC 708  
 Qy 314 rAlaLeuLeuProSerAspPheSerArgTyrPheGlnTyrGluGlySerLeuThrPr 334  
 Db 709 GTGCTGTTCCTCTGCT---TGCCGGGACTATTGGACCTACCATGGCTCTTCACACGCC 765  
 Qy 334 oProCysAlaGlnGlyValIleTrpThrValPheAsnGlnThrValMetLeuSerAlaLy 354  
 Db 766 ACCTGCGAGAGTGCATTTGTGGCTGCTACTGAAAGAGCCCATGACAGTGAAGTCTAGA 825  
 Qy 354 sGlnLeuHisThrLeuSerAspThrLeuTrpGlyProGlyAspSerArg----- 370  
 Db 826 CCAGATG---GCCAASSTGCGCAGCTGTTCCGCGCAGTGCAGAGATGAGCCCGGTGCC 882  
 Qy 371 -LeuGlnLeuAsnPheArgAlaThrGlnProLeuAsnGlyArgValIleGluAlaSerPh 390  
 Db 883 TCTGGTGGGAAATTGGCGCCCTCTCTCAGCCRMKMRGGGCGAGGGTGGTGGGGCTTCTT 942  
 Qy 390 ePro-----AlaGly-ValAspSerSerProArgAlaAlaGluProValGlnLeuAsn 408  
 Db 943 CAAGTAAGGCTCTGAGCGTCCCTCTTCGGAAGGAATTCRKCCCKGAAGAG---CCAG 999  
 Qy 408 erCysLeu 410  
 Db 1000 CTTCGCTS 1007

Search completed: February 17, 2006, 16:03:00  
 Job time : 535 secs



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